

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:30:15 ; Search time 25.7761 Seconds
(without alignments)
120.578 Million cell updates/sec

Title: US-09-641-802-6
Perfect score: 62
Sequence: 1 MPQNFYKLPQM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 422553

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	62	100.0	11	4	AAB72505	Aab72505 Colostrin
2	62	100.0	11	4	AAB59311	Aab59311 Ewe colos
3	62	100.0	11	4	AAB72251	Aab72251 Colostrin
4	62	100.0	11	4	AAB72537	Aab72537 Colostrin
5	62	100.0	11	5	AAO14582	Aao14582 Neural ce
6	62	100.0	11	5	AAM51041	Aam51041 Colostrin
7	62	100.0	11	5	AAE20233	Aae20233 Colostrin
8	62	100.0	12	4	AAB59342	Aab59342 Ewe colos
9	30	48.4	8	2	AAR60468	Aar60468 Antiproli

10	30	48.4	8	2	AAR60461	Aar60461	Antiprolif
11	30	48.4	11	2	AAR21944	Aar21944	Substance
12	30	48.4	11	2	AAW92718	Aaw92718	Human tac
13	30	48.4	15	7	ABR84651	Abr84651	Human ant
14	29	46.8	15	2	AAW00884	Aaw00884	Epstein B
15	29	46.8	15	5	ABB99000	Abb99000	Phospheno
16	29	46.8	15	5	AAE20383	Aae20383	Epstein-b
17	29	46.8	15	5	ABB08787	Abb08787	Human gly
18	29	46.8	15	6	ABR44016	Abr44016	E. coli T
19	28	45.2	7	2	AAY08887	Aay08887	C. lindem
20	28	45.2	9	2	AAY48162	Aay48162	Immunogen
21	28	45.2	11	2	AAR28392	Aar28392	Bradykini
22	28	45.2	12	3	AAV93148	Aay93148	Rat G-pro
23	28	45.2	12	4	AAB60026	Aab60026	Internali
24	28	45.2	12	4	AAG67753	Aag67753	Amino aci
25	28	45.2	12	6	ABU60819	Abu60819	Peptide p
26	28	45.2	12	6	ABP97049	Abp97049	Human RFR
27	28	45.2	12	6	ABP54416	Abp54416	Human RF
28	28	45.2	12	7	ADA88861	Ada88861	Internali
29	28	45.2	14	4	AAM97397	Aam97397	Human pep
30	28	45.2	15	2	AAR97958	Aar97958	Japan ced
31	28	45.2	18	2	AAW03529	Aaw03529	Transcrip
32	28	45.2	18	2	AAV03842	Aay03842	Activatio
33	28	45.2	18	4	AAB48367	Aab48367	Human CTF
34	28	45.2	18	4	AAB60901	Aab60901	Human CTF
35	28	45.2	18	5	ABB07299	Abb07299	Chimeric
36	28	45.2	18	5	ABB09233	Abb09233	Human Oct
37	28	45.2	18	6	ABG76153	Abg76153	Human Oct
38	27	43.5	8	5	ABB09499	Abb09499	Substance
39	27	43.5	10	4	AAB91451	Aab91451	Tachykini
40	27	43.5	11	2	AAR28445	Aar28445	Neurokini
41	27	43.5	11	2	AAR42649	Aar42649	Neurokini
42	27	43.5	11	4	AAB91409	Aab91409	Tachykini
43	27	43.5	11	5	ABB09496	Abb09496	Substance
44	27	43.5	12	2	AAW15279	Aaw15279	Salmonell
45	27	43.5	12	7	ADC36089	Adc36089	Chemokine
46	27	43.5	15	2	AAR47036	Aar47036	Apolipopr
47	27	43.5	15	2	AAR97957	Aar97957	Japan ced
48	27	43.5	17	7	ABR62371	Abr62371	Apolipopr
49	26	41.9	9	5	ABG68026	Abg68026	Human ADP
50	26	41.9	9	6	ADA24181	Ada24181	Alzheimer
51	26	41.9	9	7	ADD23602	Add23602	Breast ca
52	26	41.9	10	2	AAR67100	Aar67100	Anti-tumo
53	26	41.9	11	2	AAR80026	Aar80026	Cytotoxic
54	26	41.9	11	2	AAR84907	Aar84907	Epstein-B
55	26	41.9	11	2	AAW40849	Aaw40849	Cytotoxic
56	26	41.9	15	6	AAO26063	Aao26063	Fc region
57	26	41.9	15	6	AAO26139	Aao26139	Fc region
58	26	41.9	17	4	AAB31500	Aab31500	Amino aci
59	26	41.9	17	5	AAU88220	Aau88220	Insulin/i
60	26	41.9	17	5	AAU90738	Aau90738	Insulin/i
61	26	41.9	17	5	AAU88406	Aau88406	Insulin/i
62	26	41.9	17	6	ADA04574	Ada04574	IR/IGF-1R
63	26	41.9	17	6	ADA05280	Ada05280	Human IR
64	26	41.9	17	6	ADA05126	Ada05126	Peptide S
65	26	41.9	18	4	AAB31499	Aab31499	Amino aci
66	25	40.3	8	2	AAW82484	Aaw82484	X. riobra

67	25	40.3	8	5	AAO22366	Aao22366	Protease
68	25	40.3	9	3	AAB45576	Aab45576	Human B99
69	25	40.3	9	3	AAB45575	Aab45575	Human B99
70	25	40.3	9	5	AAG80674	Aag80674	Human tum
71	25	40.3	9	6	AAE38113	Aae38113	Human COU
72	25	40.3	10	2	AAR53039	Aar53039	Immunogen
73	25	40.3	10	2	AAR78508	Aar78508	Synthetic
74	25	40.3	10	2	AAR90852	Aar90852	AggreCAN
75	25	40.3	10	2	AAW28857	Aaw28857	HTLV-1a,c
76	25	40.3	10	3	ABP41026	Abp41026	Human HER
77	25	40.3	10	3	AAY51032	Aay51032	Human der
78	25	40.3	10	5	ABG31189	Abg31189	Rat delta
79	25	40.3	11	2	AAR28446	Aar28446	Neurokini
80	25	40.3	11	2	AAR21973	Aar21973	Cyclic su
81	25	40.3	11	2	AAR21974	Aar21974	Cyclic su
82	25	40.3	11	2	AAR42650	Aar42650	Neurokini
83	25	40.3	11	2	AAW92694	Aaw92694	Human tac
84	25	40.3	11	2	AAW92693	Aaw92693	Human tac
85	25	40.3	11	4	AAG68901	Aag68901	Human Chk
86	25	40.3	11	4	AAG68899	Aag68899	Human Chk
87	25	40.3	11	4	AAG68902	Aag68902	Human Chk
88	25	40.3	11	4	AAG70257	Aag70257	Human Chk
89	25	40.3	11	4	AAG68900	Aag68900	Human Chk
90	25	40.3	11	5	AAU85994	Aau85994	Modified
91	25	40.3	11	5	ABB05584	Abb05584	Dithiol p
92	25	40.3	11	6	AAE32247	Aae32247	Arabidops
93	25	40.3	11	7	ABR83030	Abr83030	Substance
94	25	40.3	12	2	AAR79138	Aar79138	MvlLu cel
95	25	40.3	12	2	AAR92713	Aar92713	Mink p27
96	25	40.3	12	2	AAW29723	Aaw29723	Internal
97	25	40.3	12	5	AAM52788	Aam52788	CCR5-bind
98	25	40.3	12	5	AAO22434	Aao22434	Protease
99	25	40.3	12	6	ADA50132	Ada50132	Mad2 bind
100	25	40.3	14	2	AAY41869	Aay41869	Rheumatoi

ALIGNMENTS

RESULT 1

AAB72505

ID AAB72505 standard; peptide; 11 AA.

XX

AC AAB72505;

XX

DT 09-MAY-2001 (first entry)

XX

DE Colostrinin peptide #6.

XX

KW Dermatological; oxidative stress regulator; colostrinin.

XX

OS Unidentified.

XX

PN WO200112650-A2.

XX

PD 22-FEB-2001.

XX

PF 17-AUG-2000; 2000WO-US022665.
XX
PR 17-AUG-1999; 99US-0149310P.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX
PI Stanton GJ, Hughes TK, Boldogh I;
XX
DR WPI; 2001-218342/22.
XX
PT Modulating oxidative stress level in a cell, involves contacting the cell
PT with an oxidative stress regulator selected from colostrinin, its
PT constituent peptide, analog or their combinations.
XX
PS Claim 6; Page 25; 48pp; English.
XX
CC The present invention relates to a method for modulating the oxidative
CC stress level in a cell or a patient, comprising contacting the cell with,
CC or administering to the patient, an oxidative stress regulator selected
CC from colostrinin, or its constituent peptide (e.g. the present peptide),
CC to change the level of an oxidising species in the cell. The method can
CC be used to treat oxidative damage to skin, by decreasing or preventing an
CC increase in the level of damage to a biomolecule of the patient
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 62; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFYKLPQM 11
| | | | | | | | | |
Db 1 MPQNFYKLPQM 11

RESULT 2
AAB59311

ID AAB59311 standard; peptide; 11 AA.
XX
AC AAB59311;
XX
DT 21-MAR-2001 (first entry)
XX
DE Ewe colostrinin peptide fragment A-2.
XX
KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.
XX
OS Ovis sp.
XX
PN WO200075173-A2.
XX
PD 14-DEC-2000.
XX
PF 02-JUN-2000; 2000WO-GB002128.
XX
PR 02-JUN-1999; 99GB-00012852.

XX
PA (REGE-) REGEN THERAPEUTICS PLC.
XX
PI Georgiades JA;
XX
DR WPI; 2001-071058/08.
XX
PT Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system and
PT immune system, viral and bacterial infections, and diseases characterized
PT by amyloid plaques.
XX
PS Claim 7; Page 27; 63pp; English.
XX
CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 62; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFYKLPQM 11
| | | | | | | | | |
Db 1 MPQNFYKLPQM 11

RESULT 3
AAB72251
ID AAB72251 standard; peptide; 11 AA.
XX
AC AAB72251;
XX
DT 14-MAY-2001 (first entry)
XX
DE Colostrinin derived cytokine inducing peptide SEQ ID 6.
XX
KW Colostrinin; immune response; cytokine; blood cell proliferation;
KW central nervous system disorder; neurological disorder; mental disorder;
KW dementia; neurodegenerative disease; Alzheimer's disease; psychosis;
KW neurosis; infection.
XX
OS Synthetic.
XX
PN WO200111937-A2.
XX
PD 22-FEB-2001.
XX
PF 17-AUG-2000; 2000WO-US022818.
XX

PR 17-AUG-1999; 99US-0149311P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX
 DR WPI; 2001-202804/20.
 XX
 PT Inducing a cytokine and modulating an immune response, useful for
 PT treating central nervous system diseases and bacterial and viral
 PT infections, comprises administering colostrinin as an immunological
 PT regulator.
 XX
 PS Claim 1; Page 34; 50pp; English.
 XX
 CC Sequences AAB72246 - AAB72275 represent peptides derived from clostrinin,
 CC a proline rich polypeptide aggregate contained in colostrum. The peptides
 CC have immune response modulatory activity, and are capable of inducing
 CC cytokines. Colostrinin and its derived peptides are useful for inducing
 CC cytokine production, for modulating an immunological response and for
 CC inducing blood cell proliferation. The peptides are useful in the
 CC treatment of disorders of the central nervous system, neurological
 CC disorders, mental disorders, dementia, neurodegenerative diseases,
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic
 CC disorders of the immune system, bacterial and viral infections and
 CC acquired immunological deficiencies
 XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 62; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00025;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFYKLPQM 11
 |||||
 Db 1 MPQNFYKLPQM 11

RESULT 4
 AAB72537
 ID AAB72537 standard; peptide; 11 AA.
 XX
 AC AAB72537;
 XX
 DT 09-MAY-2001 (first entry)
 XX
 DE Colostrinin peptide #6.
 XX
 KW Neuroprotective; neural cell differentiation regulator; colostrinin;
 KW colostrum.
 XX
 OS Unidentified.
 XX
 PN WO200112651-A2.
 XX
 PD 22-FEB-2001.

XX
 PF 17-AUG-2000; 2000WO-US022774.
 XX
 PR 17-AUG-1999; 99US-0149633P.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Boldogh I;
 XX
 DR WPI; 2001-226545/23.
 XX
 PT Use of colostrinin, its constituent peptide or analog as a neural cell
 PT regulator, for promoting neural cell differentiation and treating damaged
 PT neural cells in a patient.
 XX
 PS Claim 6; Page 21; 35pp; English.
 XX
 CC The present invention relates to a method for promoting neural cell
 CC differentiation and treating damaged neural cells, using colostrinin and
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum
 XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 62; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00025;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFYKLPQM 11
 |||||
 Db 1 MPQNFYKLPQM 11

RESULT 5

AAO14582

ID AAO14582 standard; peptide; 11 AA.

XX

AC AAO14582;

XX

DT 27-MAY-2002 (first entry)

XX

DE Neural cell regulatory colostrinin peptide 6.

XX

KW Neural cell differentiation; neural cell regulator; colostrinin peptide;

KW neural cell formation; proline-rich polypeptide aggregate; colostrum;

KW neural cell treatment.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Modified-site 11

FT /note= "Optional C-terminal amide"

XX

PN WO200213851-A1.

XX

PD 21-FEB-2002.

XX

PF 17-AUG-2000; 2000WO-US022777.

XX

PR 17-AUG-2000; 2000WO-US022777.

XX

PA (TEXA) UNIV TEXAS SYSTEM.

XX

PI Boldogh I, Stanton JG, Hughes TK;

XX

DR WPI; 2002-269152/31.

XX

PT Promoting cell differentiation in a patient involves use of blood cell
PT regulator selected from colostrinin, its constituent peptide and/or
PT analog.

XX

PS Claim 7; Page 21; 37pp; English.

XX

CC The invention comprises a method for promoting cell differentiation (e.g.
CC neural cell differentiation). The method involves contacting cells with a
CC neural cell regulator (i.e. a colostrinin peptide) in order to change the
CC cells in morphology to form neural cells. Colostrinin is a proline-rich
CC polypeptide aggregate that is present in colostrum. The method of the
CC invention is useful for promoting the differentiation of cells and for
CC treating damaged neural cells in a patient. The present amino acid
CC sequence represents a specifically claimed colostrinin peptide used in
CC the method of the invention

XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 62; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFYKLPQM 11
| | | | | | | | | |
Db 1 MPQNFYKLPQM 11

RESULT 6

AAM51041

ID AAM51041 standard; peptide; 11 AA.

XX

AC AAM51041;

XX

DT 30-MAY-2002 (first entry)

XX

DE Colostrinin constituent peptide.

XX

KW Colostrinin; colostrum; immunomodulator; cardiovascular;
KW blood cell regulator; cytokine inducer; human.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 11

FT /note= "optional C-terminal amidation"

XX

PN WO200213849-A1.

XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2000; 2000WO-US022775.
 XX
 PR 17-AUG-2000; 2000WO-US022775.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (REGE-) REGEN THERAPEUTICS PLC.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I, Georgiades J;
 XX
 DR WPI; 2002-269150/31.
 XX
 PT Modulation of blood cell proliferation in a patient involves use of blood
 PT cell regulator selected from colostrinin, its constituent peptide and/or
 PT analog.
 XX
 PS Claim 1; Page 34; 54pp; English.
 XX
 CC The present sequence is that of a colostrinin constituent peptide that is
 CC preferred for use as an immunological regulator and as a blood cell
 CC regulator in claimed methods of the invention. Methods are claimed for:
 CC inducing a cytokine in a cell by contact with an immunological regulator,
 CC where the cell is present in a cell culture, a tissue, an organ or an
 CC organism, and the cell is mammalian, including human; modulating an
 CC immune response in a cell by contact with the immunological regulator
 CC under conditions effective to induce a cytokine; modulating an immune
 CC response in a patient by administering an immunological regulator under
 CC conditions effective to induce a cytokine, where the immunological
 CC regulator is administered topically or as part of a dietary supplement,
 CC and where the immune response is specific or non specific, an interferon
 CC response or an antibody response; modulating blood cell proliferation by
 CC contacting blood cells with a blood cell regulator, where the blood cells
 CC are present in a cell culture or an organism, are mammalian or human, and
 CC where the blood cells are increased in number or differentiated; and a
 CC method for modulating blood cell proliferation in a patent. A claimed
 CC cytokine-inducing composition comprises a pharmaceutical carrier and an
 CC active agent such as the present peptide. Cytokines induced by this
 CC peptide in human leucocyte cultures include interferon-gamma, tumour
 CC necrosis factor-alpha, interleukin-6 and interleukin-10
 XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 62; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00025;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFYKLPQM 11
 |||||
 Db 1 MPQNFYKLPQM 11

RESULT 7
 AAE20233
 ID AAE20233 standard; peptide; 11 AA.
 XX

AC AAE20233;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Colostrinin constituent peptide #6.
 XX
 KW Blood cell regulator; colostrinin; constituent peptide; oxidative stress;
 KW therapy; oxidative damage; skin; aging; wound healing; cell replacement;
 KW tissue; organ; cosmetic procedure; repair; regeneration; preservation;
 KW transplantation; implantation; dermatological; vulnerary.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 11
 FT /note= "Optionally C-terminal amide"
 XX
 PN WO200213850-A1.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2000; 2000WO-US022776.
 XX
 PR 17-AUG-2000; 2000WO-US022776.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 XX
 PI Stanton GJ, Hughes TK, Boldogh I;
 XX
 DR WPI; 2002-269151/31.
 XX
 PT Composition useful for the modulation of blood cell proliferation in a
 PT patient comprises a blood cell regulator selected from colostrinin, its
 PT constituent peptide and/or analog.
 XX
 PS Claim 6; Page 25; 51pp; English.
 XX
 CC The invention relates to a composition which comprises a blood cell
 CC regulator selected from colostrinin, its constituent peptide and/or
 CC analogue. The invention is used for modulating the oxidative stress level
 CC in a cell e.g. mammalian or human cell present in a cell culture, tissue,
 CC organ, or organism; or for treating oxidative damage to the skin of a
 CC patient e.g. animal or human; to modulate oxidative stress during/ after
 CC a premature birth or normal birth, preventing/delaying aging in a
 CC patient, enhancing wound healing, and the reduction of side effects of
 CC cosmetic procedures. The method changes the level of an oxidising species
 CC in the cell, such as decreases or prevents increase in the level of
 CC damage to a biomolecule of the patient selected from DNA, protein and/or
 CC lipid, compared to the same conditions when the oxidative stress
 CC regulator is not present. The modulation of oxidative stress results in
 CC enhanced repair, regeneration, and replacement of cells, tissues and
 CC organs (e.g. kidney, liver, pancreas, skin, and the other internal and
 CC external organs), as well as enhanced preservation of such organs for
 CC transplantation, implantation, or scientific research. The present
 CC sequence is a colostrinin constituent peptide
 XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 62; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFYKLPQM 11
|||||||
Db 1 MPQNFYKLPQM 11

RESULT 8

AAB59342

ID AAB59342 standard; peptide; 12 AA.

XX

AC AAB59342;

XX

DT 21-MAR-2001 (first entry)

XX

DE Ewe colostrinin peptide fragment derived sequence #2.

XX

KW Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;
KW central nervous system disorder; dietary supplement; beta-amyloid plaque.

XX

OS Ovis sp.

XX

PN WO200075173-A2.

XX

PD 14-DEC-2000.

XX

PF 02-JUN-2000; 2000WO-GB002128.

XX

PR 02-JUN-1999; 99GB-00012852.

XX

PA (REGE-) REGEN THERAPEUTICS PLC.

XX

PI Georgiades JA;

XX

DR WPI; 2001-071058/08.

XX

PT Peptides having an N-terminal amino acid sequence isolated from
PT colostrinin for treating e.g. disorders of the central nervous system and
PT immune system, viral and bacterial infections, and diseases characterized
PT by amyloid plaques.

XX

PS Claim 8; Page 27; 63pp; English.

XX

CC The present invention provides the sequences of a number of peptides
CC found in ewe's colostrinin. Colostrinin is the proline-rich polypeptide
CC fragment of colostrum. These peptides can be used in the treatment of
CC central nervous system disorders such as senile dementia, Parkinson's
CC disease, Alzheimer's disease, psychosis and neurosis, immune system
CC disorders such as bacterial and viral infections, to improve the
CC development of a child's immune system, as a dietary supplement, and to
CC promote the dissolution of beta-amyloid plaques

XX

SQ Sequence 12 AA;

Query Match 100.0%; Score 62; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFYKLPQM 11
 |||||||
Db 2 MPQNFYKLPQM 12

RESULT 9

AAR60468

ID AAR60468 standard; peptide; 8 AA.

XX

AC AAR60468;

XX

DT 25-MAR-2003 (revised)

DT 30-MAR-1995 (first entry)

XX

DE Antiproliferative peptide to transplantable human B-cell lymphoma.

XX

KW antiproliferative; transplant; B-cell lymphoma line SUP-B8; Burkitt's;

KW inhibit clonal expansion; induce apoptosis; anti-idiotypic; IgM lambda;

KW inhibit cell proliferation; peptidomimetics; cell surface receptor;

KW immunoglobulin superfamily; treatment; neoplasia; identification;

KW induce replication; therapy; clonal anergy; modulate tyrosine kinase.

XX

OS Synthetic.

XX

PN WO9418345-A1.

XX

PD 18-AUG-1994.

XX

PF 04-FEB-1994; 94WO-US001319.

XX

PR 05-FEB-1993; 93US-00014426.

PR 15-NOV-1993; 93US-00153341.

XX

PA (AFFY-) AFFYMAX TECHNOLOGIES NV.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

XX

PI Renschler MF, Levy R, Bhatt RR, Dower WJ;

XX

DR WPI; 1994-279762/34.

XX

PT Identifying anti-proliferative peptide(s) which specifically bind to
PT immunoglobulin super-family species idioype - esp. to inhibit B-cell
PT lymphoma and leukocytic leukaemia cell proliferation, for anti-idiotypic
PT therapy.

XX

PS Claim 7; Page 45; 69pp; English.

XX

CC AAR60400-73 are peptide ligands which bind to purified IgM lambda
CC receptor of the human Burkitt's lymphoma cell line SUP-B8. Peptides
CC AAR60414 to AAR60473 were biotinylated and linked to streptavidin. The
CC peptides were identified with the use of filamentous phage libraries
CC displaying random peptides. Corresponding synthetic peptides bound
CC specifically to this Ig receptor, and blocked the binding of an anti-

CC idiotypic antibody. The ligands, when conjugated to form dimers or
CC tetramers, induced cell death by apoptosis in vitro at nanomolar
CC concentrations. This effect was associated with the specific stimulation
CC of intracellular protein tyrosine phosphorylation. The peptides of the
CC invention can be used individually, as complexes of cross-linked peptides
CC or can be conjugated to deliver toxins or radionuclides to neoplastic
CC cells bearing the specific Ig receptor. (Updated on 25-MAR-2003 to
CC correct PN field.)

XX

SQ Sequence 8 AA;

Query Match 48.4%; Score 30; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFYK 7

||::||:

Db 1 MPEDFYR 7

RESULT 10

AAR60461

ID AAR60461 standard; peptide; 8 AA.

XX

AC AAR60461;

XX

DT 25-MAR-2003 (revised)

DT 30-MAR-1995 (first entry)

XX

DE Antiproliferative peptide to transplantable human B-cell lymphoma.

XX

KW antiproliferative; transplant; B-cell lymphoma line SUP-B8; Burkitt's;

KW inhibit clonal expansion; induce apoptosis; anti-idiotypic; IgM lambda;

KW inhibit cell proliferation; peptidomimetics; cell surface receptor;

KW immunoglobulin superfamily; treatment; neoplasia; identification;

KW induce replication; therapy; clonal anergy; modulate tyrosine kinase.

XX

OS Synthetic.

XX

PN WO9418345-A1.

XX

PD 18-AUG-1994.

XX

PF 04-FEB-1994; 94WO-US001319.

XX

PR 05-FEB-1993; 93US-00014426.

PR 15-NOV-1993; 93US-00153341.

XX

PA (AFFY-) AFFYMAX TECHNOLOGIES NV.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

XX

PI Renschler MF, Levy R, Bhatt RR, Dower WJ;

XX

DR WPI; 1994-279762/34.

XX

PT Identifying anti-proliferative peptide(s) which specifically bind to

PT immunoglobulin super-family species idiotypic - esp. to inhibit B-cell

PT lymphoma and leukocytic leukaemia cell proliferation, for anti-idiotypic
PT therapy.
XX
PS Claim 7; Page 45; 69pp; English.
XX
CC AAR60400-73 are peptide ligands which bind to purified IgM lambda
CC receptor of the human Burkitt's lymphoma cell line SUP-B8. Peptides
CC AAR60414 to AAR60473 were biotinylated and linked to streptavidin. The
CC peptides were identified with the use of filamentous phage libraries
CC displaying random peptides. Corresponding synthetic peptides bound
CC specifically to this Ig receptor, and blocked the binding of an anti-
CC idiotype antibody. The ligands, when conjugated to form dimers or
CC tetramers, induced cell death by apoptosis in vitro at nanomolar
CC concentrations. This effect was associated with the specific stimulation
CC of intracellular protein tyrosine phosphorylation. The peptides of the
CC invention can be used individually, as complexes of cross-linked peptides
CC or can be conjugated to deliver toxins or radionuclides to neoplastic
CC cells bearing the specific Ig receptor. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 8 AA;

Query Match 48.4%; Score 30; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFYK 7
||::||:
Db 1 MPEDFYR 7

RESULT 11
AAR21944
ID AAR21944 standard; protein; 11 AA.
XX
AC AAR21944;
XX
DT 25-JUN-1992 (first entry)
XX
DE Substance P [Pro 11].
XX
KW Tachykinin agonist; beta-amyloid; Alzheimer's disease; Down's; syndrome;
KW hereditary cerebral haemorrhage.
XX
OS Synthetic.
XX
PN WO9202248-A.
XX
PD 20-FEB-1992.
XX
PF 27-JUL-1990; 90US-00559173.
XX
PR 27-JUL-1990; 90US-00559173.
XX
PA (CHIL-) CHILDRENS MED CENT.
XX
PI Yankner BA;

XX
 DR WPI; 1992-079804/10.
 XX
 PT Treatment of neuronal accumulation of beta-amyloid - using tachykinin
 PT agonists e.g. substance P, physalaemin and neurokinin B, for treating
 PT alzheimer's disease, downs syndrome, etc.
 XX
 PS Claim 10; Page 21; 35pp; English.
 XX
 CC The peptide is the tachykinin agonist substance P with a Proline residue
 CC substituted at position 11. The peptide was synthesised by standard solid
 CC phase synthesis. Neuronal accumulation of beta-amyloid may be treated by
 CC administration of tachykinin agonists. The peptide can reduce the
 CC neurotoxic effects of a beta-amyloid related polypeptide on cultured
 CC neurons. The peptide and its analogues are useful for controlling
 CC diseases characterised by beta amyloid accumulation in the brain such as
 CC Alzheimer's disease and Down's syndrome. See also AAR21932-75
 XX
 SQ Sequence 11 AA;

Query Match 48.4%; Score 30; DB 2; Length 11;
 Best Local Similarity 62.5%; Pred. No. 1.3e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFKYKLP 9
 || |: ||
 Db 4 PQQFFGLP 11

RESULT 12
 AAW92718

ID AAW92718 standard; peptide; 11 AA.
 XX
 AC AAW92718;
 XX
 DT 20-MAR-2003 (revised)
 DT 30-APR-1999 (first entry)
 XX
 DE Human tachykinin agonist beta-amyloid peptide fragment #64.
 XX
 KW Tachykinin agonist; beta-amyloid; inhibition; neurotoxin; treatment;
 KW Alzheimer's disease; Down's syndrome; amyloidosis; human;
 KW hereditary cerebral haemorrhage; non-inherited congophilic angiopathy.
 XX
 OS Homo sapiens.
 XX
 PN US5876948-A.
 XX
 PD 02-MAR-1999.
 XX
 PF 29-JUL-1991; 91US-00737371.
 XX
 PR 27-JUL-1990; 90US-00559173.
 XX
 PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX
 PI Yankner BA;

XX
 DR WPI; 1999-189630/16.
 XX
 PT Screening for neurotoxin inhibitors - by testing compounds for their
 PT effect on beta-amyloid peptide neurotoxic effect on neuronal cells.
 XX
 PS Disclosure; Col 37-38; 28pp; English.
 XX
 CC This invention describes a method for screening compounds for inhibiting
 CC a neurotoxin. The method involves incubating tachykinin agonists with
 CC neuronal cells and a beta-amyloid peptide neurotoxin. The methods can be
 CC used for identifying compounds for treating diseases characterised by an
 CC undesirable build up of beta-amyloid protein, e.g. Alzheimer's disease,
 CC Down's syndrome, and the syndromes of hereditary cerebral haemorrhage
 CC with amyloidosis and non-inherited congophilic angiopathy with cerebral
 CC haemorrhage. AAW92655-W92731 are tachykinin agonists derived from human
 CC beta-amyloid peptide fragments. (Updated on 20-MAR-2003 to correct PF
 CC field.)
 XX
 SQ Sequence 11 AA;

Query Match 48.4%; Score 30; DB 2; Length 11;
 Best Local Similarity 62.5%; Pred. No. 1.3e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKLP 9
 || |: ||
 Db 4 PQQFFGLP 11

RESULT 13

ABR84651

ID ABR84651 standard; peptide; 15 AA.

XX

AC ABR84651;

XX

DT 18-DEC-2003 (first entry)

XX

DE Human antigenic SGA-1M peptide fragment #1.

XX

KW Human; SGA-1M; cancer; antigen; cytostatic; breast cancer;

KW ovarian cancer; skin cancer; lymphoid system; thyroid cancer;

KW pancreatic cancer; stomach cancer; lung cancer.

XX

OS Homo sapiens.

XX

PN WO2003065873-A2.

XX

PD 14-AUG-2003.

XX

PF 03-FEB-2003; 2003WO-US002974.

XX

PR 01-FEB-2002; 2002US-0353826P.

XX

PA (SEAT-) SEATTLE GENETICS INC.

XX

PI Petroziello JM, Law C, Wahl AF;

XX
 DR WPI; 2003-731465/69.
 XX
 PT Diagnosing or staging cancer in a subject by detecting or measuring a SGA
 PT -1M gene product in a sample derived from the subject.
 XX
 PS Example; Page 184; Opp; English.
 XX
 CC The present invention relates to a method of diagnosing or staging cancer
 CC in a subject, which comprises detecting or measuring a SGA-1M gene
 CC product in a sample derived from the subject, where elevated levels of
 CC the SGA-1M gene product compared to a non-cancerous sample or
 CC predetermined standard value for a noncancerous sample indicates the
 CC presence or advanced stage of cancer in the subject. Also provided is the
 CC human SGA-1M gene, its two open reading frames and the two encoded
 CC proteins. The method is useful for diagnosing or staging cancer in a
 CC subject, and comprises detecting or measuring a SGA-1M gene product in a
 CC sample derived from the subject, where elevated levels of the SGA-1M gene
 CC product compared to a non-cancerous sample or predetermined standard
 CC value for a noncancerous sample indicates the presence or advanced stage
 CC of cancer. The SGA-1M gene product is also useful for vaccinating a
 CC subject against cancer. It is particularly linked to breast, ovarian,
 CC skin, thyroid, pancreatic, stomach and lung cancer, and cancers of the
 CC lymphoid system. The present sequence is a fragment of the protein of the
 CC invention
 XX
 SQ Sequence 15 AA;

Query Match 48.4%; Score 30; DB 7; Length 15;
 Best Local Similarity 50.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPQNFYKLPQ 10
 ||: | ||:
 Db 5 MPETFSNLPR 14

RESULT 14

AAW00884

ID AAW00884 standard; peptide; 15 AA.

XX

AC AAW00884;

XX

DT 27-AUG-2003 (revised)

DT 23-MAY-1997 (first entry)

XX

DE Epstein Barr virus EBNA-2 p276-290.

XX

KW Adeno-associated virus; vector; liposome; transfection; dendritic cell;

KW EBV; EBNA-2; adoptive immunotherapy; tumour associated antigen.

XX

OS Human herpesvirus 4.

XX

PN W09703703-A1.

XX

PD 06-FEB-1997.

XX

PF 19-JUL-1996; 96WO-US012012.
 XX
 PR 21-JUL-1995; 95US-0001312P.
 PR 01-NOV-1995; 95US-0007184P.
 PR 01-DEC-1995; 95US-00566286.
 XX
 PA (RHON) RHONE POULENC RORER PHARM INC.
 XX
 PI Philip R, Lebkowski JS;
 XX
 DR WPI; 1997-145208/13.
 XX
 PT Adeno-associated virus:liposome complexes for transfecting dendritic
 PT cells - for inducing immune response, useful for treating e.g. neoplasia
 PT or infections.
 XX
 PS Example 5; Page 58; 134pp; English.
 XX
 CC Tumour associated antigens (AAW13660-61, AAW00878-903) can be loaded into
 CC dendritic cells and used to induce antitumour immunity. Alternatively,
 CC the dendritic cells are transfected with adeno associated virus plasmid
 CC DNA (which includes DNA encoding the tumour associated antigen) complexed
 CC with cationic liposomes. The antigen loaded or transfected dendritic
 CC cells can be used to generate tumour antigen-specific cytotoxic T
 CC lymphocytes for use in adoptive immunotherapy in a patient having the
 CC corresponding tumour. A suitable antigen comprises amino acids 276-290
 CC (AAW00884) of Epstein Barr virus EBNA-2. (Updated on 27-AUG-2003 to
 CC correct OS field.)
 XX
 SQ Sequence 15 AA;

Query Match 46.8%; Score 29; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PQNFYKLPQM 11
 | ||:| |
 Db 4 PTVFYNIIPPM 13

RESULT 15
 ABB99000
 ID ABB99000 standard; peptide; 15 AA.
 XX
 AC ABB99000;
 XX
 DT 14-APR-2003 (first entry)
 XX
 DE Phosphoenol pyruvate dependent glycosylphosphate transferase 9.02 peptide.
 XX
 KW Phosphoenol pyruvate dependent glycosylphosphate transferase 9.02; cancer;
 KW cytostatic; HIV infection; anti-HIV; enzyme.
 XX
 OS Unidentified.
 XX
 PN CN1363668-A.
 XX

PD 14-AUG-2002.
 XX
 PF 05-JAN-2001; 2001CN-00105052.
 XX
 PR 05-JAN-2001; 2001CN-00105052.
 XX
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-751782/82.
 XX
 PT Polypeptide-phosphoenolpyruvate-dependent glycosylphosphate transferase
 PT 9.02 and polynucleotide for coding it.
 XX
 PS Example 5; Page 20 (Disclosure); 33pp; Chinese.
 XX
 CC The present invention relates to phosphenol pyruvate dependent
 CC glycosylphosphate transferase 9.02 (see ABB98999). The protein can be
 CC used for treating diseases such as cancer and HIV infection. The present
 CC sequence is an N-terminal peptide fragment of the protein, which was used
 CC in an example from the invention
 XX
 SQ Sequence 15 AA;

Query Match 46.8%; Score 29; DB 5; Length 15;
 Best Local Similarity 40.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MPQNFYKLPO 10
 |||:::|
 Db 1 MPANYFQIVQ 10

RESULT 16

AAE20383

ID AAE20383 standard; peptide; 15 AA.

XX

AC AAE20383;

XX

DT 07-AUG-2003 (revised)

DT 18-JUN-2002 (first entry)

XX

DE Epstein-barr virus tumour associated antigen (TAA) peptide epitope #2.

XX

KW Gene-delivery compound; single-chain binding polypeptide; SCBP;

KW nucleic acid-binding moiety; NABM; lipid-associating moiety; LAM;

KW gene therapy; targetted gene delivery; tumour associated antigen; TAA;

KW epitope.

XX

OS Cercopithecine herpesvirus 15.

XX

PN WO200200914-A2.

XX

PD 03-JAN-2002.

XX

PF 25-JUN-2001; 2001WO-US020182.

XX
PR 23-JUN-2000; 2000US-0213653P.
XX
PA (HUST/) HUSTON J S.
PA (WILS/) WILS P.
PA (QUAN/) QUAN Z.
PA (LAUR/) LAURENT O.
PA (MARA/) MARASCO W A.
PA (SCHE/) SCHERMAN D.
XX
PI Huston JS, Wils P, Quan Z, Laurent O, Marasco WA, Scherman D;
XX
DR WPI; 2002-268789/31.
XX
PT Gene-delivery compound for targeted gene delivery, comprises single-chain
PT binding polypeptide having effector segment with cysteinyl residue and
PT nucleic acid-binding/lipid-associating moiety coupled to polypeptide by
PT residue.
XX
PS Disclosure; Page 28; 96pp; English.
XX
CC The invention relates to gene-delivery compound comprising a single-chain
CC binding polypeptide (SCBP) having at least one effector segment having a
CC cysteinyl residue, and a nucleic acid-binding moiety (NABM) or a lipid-
CC associating moiety (LAM) coupled to SCBP by the residue. Gene-delivery
CC compound is useful for targetted gene delivery for treating diseases by
CC gene therapy. The present sequence is Epstein-barr virus tumour
CC associated antigen (TAA) peptide epitope. TAA may be targetted by the
CC SCBP of the present invention. (Updated on 07-AUG-2003 to correct OS
CC field.)
XX
SQ Sequence 15 AA;

Query Match 46.8%; Score 29; DB 5; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PQNFYKLPQM 11
| || :| |
Db 4 PTVFYNIIPM 13

RESULT 17
ABB08787
ID ABB08787 standard; peptide; 15 AA.
XX
AC ABB08787;
XX
DT 22-MAY-2002 (first entry)
XX
DE Human glycosyl-phosphatidyl inositol glycan F10.89 peptide.
XX
KW Human; glycosyl-phosphatidyl inositol glycan F10.89;
KW embryonic development malformation; immunological dysfunction;
KW hormonal metabolic disturbance.
XX
OS Homo sapiens.

XX
 PN CN1326960-A.
 XX
 PD 19-DEC-2001.
 XX
 PF 05-JUN-2000; 2000CN-00116326.
 XX
 PR 05-JUN-2000; 2000CN-00116326.
 XX
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2002-206969/27.
 XX
 PT New polypeptide-glycosyl-phosphatidyl inositol glycan F10.89 and
 PT polynucleotide encoding the polypeptide.
 XX
 PS Example 5; Page 20 (Disclosure); 35pp; Chinese.
 XX
 CC The invention relates to human glycosyl-phosphatidyl inositol glycan
 CC F10.89, the polynucleotide encoding this polypeptide and DNA recombinant
 CC processes to produce the polypeptide. The present invention also
 CC discloses the method of applying the polypeptide in treating various
 CC diseases, such as embryonic development malformation, immunological
 CC dysfunction disease and hormonal metabolic disturbance disease. The
 CC present invention also discloses the antagonist for resisting the
 CC polypeptide and its treatment effect. The present invention also
 CC discloses the application of the polynucleotide for encoding glycosyl-
 CC phosphatidyl inositol glycan F10.89. The present sequence is that of the
 CC N-terminal peptide from human glycosyl-phosphatidyl inositol glycan
 CC F10.89, useful in examples of the invention
 XX
 SQ Sequence 15 AA;

 Query Match 46.8%; Score 29; DB 5; Length 15;
 Best Local Similarity 71.4%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 QY 5 FYKLPQM 11
 | | : | | |
 Db 9 FVKIPQM 15

RESULT 18

ABR44016

ID ABR44016 standard; peptide; 15 AA.

XX

AC ABR44016;

XX

DT 04-AUG-2003 (first entry)

XX

DE E. coli TNase N-terminal fragment.

XX

KW Bacterium; L-cysteine; cystathionine-beta-lyase; drug; cosmetic; food;

KW TNase; enzyme.

XX

OS Escherichia coli.
 XX
 PN EP1298200-A2.
 XX
 PD 02-APR-2003.
 XX
 PF 17-SEP-2002; 2002EP-00020588.
 XX
 PR 28-SEP-2001; 2001JP-00302008.
 XX
 PA (AJIN) AJINOMOTO CO INC.
 XX
 PI Takagi H, Wada M, Nakamori S;
 XX
 DR WPI; 2003-423253/40.
 XX
 PT New bacterium belonging to genus Escherichia which is modified so that
 PT cystathionine-beta-lyase activity is reduced/eliminated, useful for
 PT producing L-cysteine useful in the field of drugs, cosmetics and foods.
 XX
 PS Example 1; Page 10; 28pp; English.
 XX
 CC The invention relates to a bacterium belonging to the genus Escherichia
 CC which has the ability to produce L-cysteine and which is modified so that
 CC cystathionine-beta-lyase activity is reduced or eliminated. The bacterium
 CC is useful for producing L-cysteine which is useful in the field of drugs,
 CC cosmetics and foods. The present sequence represents an E. coli TNase N-
 CC terminal fragment
 XX
 SQ Sequence 15 AA;

Query Match 46.8%; Score 29; DB 6; Length 15;
 Best Local Similarity 55.6%; Pred. No. 2.6e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 QNFYKLPQM 11
 :|| ||:|
 Db 2 ENFKHLPQM 10

RESULT 19
 AAY08887

ID AAY08887 standard; protein; 7 AA.
 XX
 AC AAY08887;
 XX
 DT 19-AUG-1999 (first entry)
 XX
 DE C. lindemuthianum chitin deacetylase C-terminal fragment.
 XX
 KW Chitin deacetylase; N-acetyl aminosugar; hypotensive; antibacterial;
 KW anti-osteoporotic; antitumour; cholesterol reduction; chitin; chitosan;
 KW food; animal feed; thickener; blood pressure; treatment; osteoporosis;
 KW gout; hyperuricacidemia; Bifidus bacteria.
 XX
 OS Colletotrichum lindemuthianum.
 XX

PN DE19810349-A1.
 XX
 PD 10-JUN-1999.
 XX
 PF 10-MAR-1998; 98DE-01010349.
 XX
 PR 02-DEC-1997; 97JP-00345737.
 XX
 PA (NORQ) NAT FOOD RES INST MIN AGRIC.
 XX
 PI Hamamatsu S, Hayashi K, Tokuyasu K, Mori Y;
 XX
 DR WPI; 1999-338951/29.
 XX
 PT Nucleic acid encoding bacterial chitin deacetylase useful for generating
 PT chitosan.
 XX
 PS Example 1; Page 5; 14pp; German.
 XX
 CC This invention describes a novel protein and its encoding nucleic acid
 CC deacetylase activity on the N-acetyl group of N-acetyl aminosugars which
 CC has been isolated from Colletotrichum lindemuthianum. The protein of the
 CC invention has hypotensive, antibacterial, anti-osteoporotic, antitumour
 CC and cholesterol reducing activity. The products of the invention can be
 CC used to convert chitin to chitosan. Chitosan is used in foods or animal
 CC feeds, particularly as a thickener, and in pharmaceuticals, to reduce
 CC cholesterol levels or blood pressure, in treatment of gout,
 CC hyperurinaemia and osteoporosis; for stimulating growth of Bifidus
 CC bacteria while suppressing Escherichia coli and Clostridium perfringens,
 CC and as antitumour agent. The protein of the invention is also used to
 CC produce chitosan oligosaccharides from chitin oligosaccharides and for
 CC removing N-acetyl from other amino sugars, making it suitable for
 CC synthesis of new sugar chains
 XX
 SQ Sequence 7 AA;

Query Match 45.2%; Score 28; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQNFYK 7
 |:|:|
 Db 1 PENWYK 6

RESULT 20
 AAY48162
 ID AAY48162 standard; peptide; 9 AA.
 XX
 AC AAY48162;
 XX
 DT 01-DEC-1999 (first entry)
 XX
 DE Immunogenic peptide having a human leukocyte antigen binding motif #2773.
 XX
 KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;

KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9945954-A1.
 XX
 PD 16-SEP-1999.
 XX
 PF 13-MAR-1998; 98WO-US005039.
 XX
 PR 13-MAR-1998; 98WO-US005039.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
 XX
 DR WPI; 1999-551214/46.
 XX
 PT New immunogenic peptides with HLA binding motif, useful in treatment and
 PT diagnosis of cancers and viral diseases.
 XX
 PS Claim 1; Page 140; 150pp; English.
 XX
 CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also known
 CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
 CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
 CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
 CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
 CC (CTLs) which destroy antigen-bearing cells are normally induced by an
 CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
 CC than the intact foreign antigen itself, and are particularly important in
 CC tumour rejection and in fighting viral infections. The peptides are
 CC therefore useful therapeutically to treat or prevent viral infections and
 CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
 CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
 CC elicit an immune response in individuals susceptible or otherwise at risk
 CC of viral infection or cancer, or used to treat chronic or acute
 CC conditions. They are also useful diagnostically, and can be used to
 CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
 CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
 CC patient. The polynucleotides encoding the immunogenic peptides are also
 CC useful therapeutically and for immunisation as above
 XX
 SQ Sequence 9 AA;

Query Match 45.2%; Score 28; DB 2; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
 ||| ||
 Db 2 PQNLYTL 8

RESULT 21

AAR28392

ID AAR28392 standard; peptide; 11 AA.

XX

AC AAR28392;

XX

DT 25-MAR-2003 (revised)

DT 18-MAR-1993 (first entry)

XX

DE Bradykinin receptor antagonist CT-0008.

XX

KW Bradykinin receptor antagonist; heterodimer; higher oligomer; potency;

KW duration; CP-0088; burns; migraine; shock CNS injury; asthma; rhinitis;

KW premature labour; inflammatory arthritis; homodimer;

KW inflammatory bowel disease.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 1

FT /note= "D-form residue"

FT Misc-difference 2

FT /note= "D-form residue"

FT Misc-difference 7

FT /note= "D-form residue"

FT Misc-difference 9

FT /note= "D-form residue"

FT Modified-site 11

FT /label= Nle

XX

PN WO9217201-A1.

XX

PD 15-OCT-1992.

XX

PF 30-MAR-1992; 92WO-US002431.

XX

PR 01-APR-1991; 91US-00677391.

PR 27-MAR-1992; 92US-00859582.

XX

PA (CORT-) CORTECH INC.

XX

PI Cheronis JC, Blodgett JK, Whalley ET, Eubanks SR, Allen LG;

PI Nguyen KT;

XX

DR WPI; 1992-365995/44.

XX

PT Bradykinin antagonists comprising linked bradykinin antagonist chains -

PT are for treatment of post-operative pain, asthma and aseptic shock.

XX

PS Disclosure; Page 76; 109pp; English.

XX

CC The sequence given is a bradykinin receptor antagonist which can form

CC homo- or heterodimers or higher oligomers. It demonstrates greater

CC potency and/or duration of action than the parent peptide itself.

CC Bradykinin receptors antagonists such as this can be used in the

CC treatment of burns, perioperative pain, migraine and other forms of pain,

CC shock CNS injury, asthma, rhinitis, premature labour, inflammatory
CC arthritis, inflammatory bowel disease etc. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 11 AA;

Query Match 45.2%; Score 28; DB 2; Length 11;
Best Local Similarity 71.4%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
| | | | : |
Db 4 PQNFFWL 10

RESULT 22

AAAY93148

ID AAY93148 standard; peptide; 12 AA.

XX

AC AAY93148;

XX

DT 06-DEC-2000 (first entry)

XX

DE Rat G-protein coupled receptor protein rOT7T022-derived peptide #1.

XX

KW G-protein coupled receptor; human; bovine; nervous system disorder; rat;
KW mouse; somatostatin excretion.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT Modified-site 12

FT /note= "C-terminal amide"

XX

PN W0200029441-A1.

XX

PD 25-MAY-2000.

XX

PF 11-NOV-1999; 99WO-JP006283.

XX

PR 13-NOV-1998; 98JP-00323759.

PR 08-MAR-1999; 99JP-00060030.

PR 14-APR-1999; 99JP-00106812.

PR 14-JUN-1999; 99JP-00166672.

PR 04-AUG-1999; 99JP-00221640.

PR 14-SEP-1999; 99JP-00259818.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PI Watanabe T, Kikuchi K, Terao Y, Shintani Y, Hinuma S, Fukusumi S;

PI Fujii R, Hosoya M, Kitada C;

XX

DR WPI; 2000-387747/33.

XX

PT G protein coupled receptor protein and antibodies to it for treatment and
PT diagnosis of nerve diseases.

XX

PS Example 7; Page 128; 184pp; Japanese.

XX

CC The invention relates to the isolation of novel G-protein coupled
CC receptor (GPCR) genes and their encoded proteins. This sequence
CC represents a peptide derived from the rat GPCR protein clone rOT7T022 and
CC was used in an acidification rate assay. The DNAs and proteins are used
CC for the treatment, prevention and diagnosis of disorders of the nervous
CC system. The proteins and its fragments are also promoters of somatostatin
CC excretion

XX

SQ Sequence 12 AA;

Query Match 45.2%; Score 28; DB 3; Length 12;
Best Local Similarity 55.6%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPQNFYKLP 9

|| :| ||

Db 1 MPHSFANLP 9

RESULT 23

AAB60026

ID AAB60026 standard; peptide; 12 AA.

XX

AC AAB60026;

XX

DT 05-NOV-2001 (first entry)

XX

DE Internalising peptide SEQ ID NO: 41.

XX

KW Internalising peptide; transport; apoptosis; arthritis; cancer;

KW stem cell; cell differentiation; immune response stimulation;

KW HIV vaccine.

XX

OS Synthetic.

XX

PN WO200115511-A2.

XX

PD 08-MAR-2001.

XX

PF 31-AUG-2000; 2000WO-US024034.

XX

PR 01-SEP-1999; 99US-0151980P.

PR 13-MAR-2000; 2000US-0188944P.

XX

PA (UYPI-) UNIV PITTSBURGH.

XX

PI Robbins PD, Mi Z, Frizzell R, Glorioso JC, Gambotto A;

XX

DR WPI; 2001-273309/28.

XX

PT Peptides that facilitate uptake and cytoplasmic and/or nuclear transport

PT of proteins, DNA and viruses, useful, e.g. for facilitating uptake of

PT antigens in immunogenic compositions.

XX

PS Claim 1; Page 122; 129pp; English.

XX
CC The present invention provides the sequences of 75 peptides which
CC facilitate the uptake and transport of viruses, proteins and nucleic
CC acids. These internalising peptides can be used for transport into the
CC cytoplasm or the nucleus. They are useful for facilitating uptake into
CC the cell, inducing apoptosis, for example in the treatment of arthritis
CC and cancer, to expand a population of stem cells or differentiated cells,
CC to stimulate cell differentiation, facilitate the integration of AAV into
CC the genome of a cell, and to stimulate an immune response, for example in
CC the case of a HIV vaccine. The present sequence is one of the peptides of
CC the invention
XX
SQ Sequence 12 AA;

Query Match 45.2%; Score 28; DB 4; Length 12;
Best Local Similarity 44.4%; Pred. No. 3.2e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3 QNFYKLPQM 11
:|: |:|:
Db 4 KNFFWLPEL 12

RESULT 24

AAG67753

ID AAG67753 standard; peptide; 12 AA.

XX

AC AAG67753;

XX

DT 10-DEC-2001 (first entry)

XX

DE Amino acid sequence of synthetic peptide.

XX

KW Human; prolactin secretion; hypoovarianism; sperm development;
KW osteoporosis; lactation disorder; hypothyroidism; kidney failure;
KW menopause; hyperprolactinemia; pituitary tumour; diencephalon tumour;
KW menstrual disorder; stress; autoimmune disease; prolactinoma; sterility;
KW impotence; amenorrhea; lactorrhea; hyperpituitarism;
KW Sheehan's syndrome Chauri-Frommel syndrome; Argonz-del Castillo syndrome;
KW lymphoma; Forbes-Albright syndrome; spermatogenesis disorder.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 12

FT /note= "amide attached to residue"

XX

PN WO200166134-A1.

XX

PD 13-SEP-2001.

XX

PF 06-MAR-2001; 2001WO-JP001716.

XX

PR 06-MAR-2000; 2000JP-00065752.

PR 07-DEC-2000; 2000JP-00378001.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX
 PI Matsumoto Y, Watanabe T, Hinuma S, Habata Y, Yoshida H;
 XX
 DR WPI; 2001-596812/67.
 XX
 PT New polypeptide, useful as a vasotropic, tranquilizing, immunosuppressive
 PT and gynecological agent comprises the prolactin secretion regulator.
 XX
 PS Example 1; Page 94; 180pp; Japanese.
 XX
 CC The specification describes a human polypeptide which is a prolactin
 CC secretion regulating agent. The prolactin secretion regulating agent
 CC polypeptide and polynucleotide are used for the treatment and prevention
 CC of hypoovarianism, sperm under development, osteoporosis, menopause,
 CC lactation disorders, hypothyroidism, kidney failure, hyperprolactinemia,
 CC pituitary tumour, diencephalon tumour, menstrual disorders, stress,
 CC autoimmune disease, prolactinoma, sterility, impotence, amenorrhea,
 CC lactorrhea, hyperpituitarism, Chairi-Frommel syndrome, Argonz-del Castilo
 CC syndrome, Forbes-Albright syndrome, lymphoma, Sheehan's syndrome and
 CC spermatogenesis disorders. The present peptide was used in the course of
 CC the invention
 XX
 SQ Sequence 12 AA;

Query Match 45.2%; Score 28; DB 4; Length 12;
 Best Local Similarity 55.6%; Pred. No. 3.2e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPQNFYKLP 9
 || :| ||
 Db 1 MPHSFANLP 9

RESULT 25

ABU60819

ID ABU60819 standard; peptide; 12 AA.

XX

AC ABU60819;

XX

DT 06-MAY-2003 (first entry)

XX

DE Peptide production by gene recombination associated peptide #3.

XX

KW Peptide production; low-molecular peptide; KiSS-1; GPR8 ligand;

KW gene recombination.

XX

OS Homo sapiens.

XX

PN WO200292829-A1.

XX

PD 21-NOV-2002.

XX

PF 16-MAY-2002; 2002WO-JP004735.

XX

PR 17-MAY-2001; 2001JP-00147341.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX
 PI Nishimura O, Suenaga M, Ito T, Kitada C;
 XX
 DR WPI; 2003-129302/12.
 XX
 PT Process for producing peptides e.g. KiSS-1 peptide and GPR8 ligand for
 PT subsequent applications by gene recombination technique through tandem
 PT repeats to provide precursor protein with specific cleavage sites.
 XX
 PS Disclosure; Page 52; 87pp; Japanese.
 XX
 CC The invention describes a method of producing a peptide comprising the
 CC excision of the N and C-terminals of a target peptide with enzymes or
 CC chemically through the attached cleavage sites repeated by ligation in a
 CC precursor protein. The method is for producing (low-molecular) peptides
 CC e.g. KiSS-1 peptide and GPR8 ligand for subsequent applications by the
 CC gene recombination technique through tandem repeats to provide a
 CC precursor protein with specific cleavage sites. With this method, peptide
 CC production can be carried out easily to provide large quantities of the
 CC required peptides. This is the amino acid sequence of a peptide
 CC associated with the peptide production method of the invention
 XX
 SQ Sequence 12 AA;

Query Match 45.2%; Score 28; DB 6; Length 12;
 Best Local Similarity 55.6%; Pred. No. 3.2e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPQNFYKLP 9
 || :| ||
 Db 1 MPHSEFANLP 9

RESULT 26

ABP97049

ID ABP97049 standard; peptide; 12 AA.

XX

AC ABP97049;

XX

DT 23-JUN-2003 (first entry)

XX

DE Human RFRP-3 peptide SEQ ID NO:39.

XX

KW RFRP-3; prolactin secretion promoter; secretion; prolactin; GPCR;

KW G protein-coupled receptor; gynaecological; osteopathic; cytostatic;

KW immunomodulator; antiinfertility; vasotropic; hypoovarianism; menopause;

KW prolactin secretion-related disease; spermatoc hypoplasia.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 12

FT /label= amidated

XX

PN WO2003018795-A1.

XX

PD 06-MAR-2003.

XX
 PF 22-AUG-2002; 2002WO-JP008466.
 XX
 PR 24-AUG-2001; 2001JP-00254826.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Hinuma S, Yoshida H, Habata Y, Hosoya M, Kitada C;
 XX
 DR WPI; 2003-268422/26.
 DR N-PSDB; ACC49304.
 XX
 PT Novel RFRP-3 peptides and encoded DNAs, applicable in diagnosis of and
 PT developing drugs for treating prolactin secretion-related diseases e.g.
 PT hypoovarianism, spermatoc hypoplasia and menopause.
 XX
 PS Example; Page 107; 197pp; Japanese.
 XX
 CC The present invention describes RFRP-3 peptides. RFRP-3 is a G protein-
 CC coupled receptor (GPCR) which is a prolactin secretion promoter. RFRP-3
 CC has gynaecological, osteopathic, cytostatic, immunomodulator, vasotropic
 CC and antiinfertility activities. The RFRP-3 peptides and their encoded
 CC DNAs can be used in the diagnosis of and developing drugs for treating
 CC prolactin secretion-related diseases e.g. hypoovarianism, spermatoc
 CC hypoplasia and menopause. The developed drugs are safe with low toxicity.
 CC The present sequence represents a human RFRP-3 peptide, which is used in
 CC the exemplification of the present invention
 XX
 SQ Sequence 12 AA;

Query Match 45.2%; Score 28; DB 6; Length 12;
 Best Local Similarity 55.6%; Pred. No. 3.2e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPQNFYKLP 9
 || :| ||
 Db 1 MPHSFANLP 9

RESULT 27

ABP54416

ID ABP54416 standard; peptide; 12 AA.

XX

AC ABP54416;

XX

DT 21-JAN-2003 (first entry)

XX

DE Human RF amide peptide related sequence SEQ ID NO:3.

XX

KW Rf amide peptide; cytostatic; antiinfertility; prolactin-related disease;

KW hyperprolactinemia; infertility; Chiari-Frommel syndrome; cancer;

KW Forbes-Albright syndrome.

XX

OS Homo sapiens.

XX

PN WO200246405-A1.

XX

PD 13-JUN-2002.
 XX
 PF 06-DEC-2001; 2001WO-JP010668.
 XX
 PR 07-DEC-2000; 2000JP-00373125.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Suenaga M, Yamada T, Nishimura O;
 XX
 DR WPI; 2003-018538/01.
 DR N-PSDB; ABQ83409.
 XX
 PT Producing an RF amide peptide for treating prolactin-related diseases,
 PT comprises obtaining a fusion protein or peptide using a transformant then
 PT cleaving the peptide bond in the amino acid side of a cysteine residue.
 XX
 PS Claim 6; Page 81; 100pp; Japanese.
 XX
 CC The present invention describes a method for producing an RF amide
 CC peptide (I) which can be a partial peptide of a polypeptide selected from
 CC the amino acid sequences given in ABP5442 to ABP54427, by cleaving a
 CC peptide bond in the amino acid side of the cysteine residue of a fusion
 CC protein or polypeptide linked to the N-terminal of a protein or
 CC polypeptide with cysteine at its N-terminal and optionally an oxidisable
 CC methionine residue. (I) has cytostatic and antiinfertility activities.
 CC The method can be used for producing a peptide which is used for
 CC preventing or treating prolactin-related diseases, e.g.
 CC hyperprolactinemia, infertility, Chiari-Frommel syndrome, Forbes-Albright
 CC syndrome and cancer. The method is used for large-scale industrial
 CC production of the peptide. The present sequence represents a specifically
 CC claimed peptide from the present invention
 XX
 SQ Sequence 12 AA;

Query Match 45.2%; Score 28; DB 6; Length 12;
 Best Local Similarity 55.6%; Pred. No. 3.2e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPQNFYKLP 9
 || :| ||
 Db 1 MPHSEFANLP 9

RESULT 28

ADA88861

ID ADA88861 standard; peptide; 12 AA.

XX

AC ADA88861;

XX

DT 20-NOV-2003 (first entry)

XX

DE Internalised peptide pep35 SEQ ID NO:41.

XX

KW internalising peptide; cytostatic; antiinflammatory; immunomodulator;

KW antiarthritic; cytoplasmic transport; nuclear transport;

KW peptide-cargo complex; apoptosis; arthritic; tumour; differentiation;

KW immune response; vaccine; inflammation; necrosis; transplantation;
 KW cystic fibrosis; lung inflammation; gene therapy.
 XX
 OS Synthetic.
 XX
 PN WO2003068942-A2.
 XX
 PD 21-AUG-2003.
 XX
 PF 12-FEB-2003; 2003WO-US004632.
 XX
 PR 13-FEB-2002; 2002US-00075869.
 XX
 PA (UYPI-) UNIV PITTSBURGH.
 XX
 PI Robbins PD, Mi Z, Frizzel R, Glorioso JC, Gambotto A, Mai JC;
 XX
 DR WPI; 2003-697526/66.
 XX
 PT New internalizing peptides, useful for facilitating the delivery, uptake
 PT and cytoplasmic and/or nuclear transport of proteins, DNA or viruses into
 PT a target cell, for inducing apoptosis in arthritic or tumor cells, or in
 PT gene therapy.
 XX
 PS Example 3; Page 19; 17lpp; English.
 XX
 CC The present invention describes an internalising peptide (I) comprising
 CC any one of 14 fully defined amino acid sequences (designated P1-P14, see
 CC ADA88896 to ADA88906, and ADA88917 to ADA88919). (I) has cytostatic,
 CC antiinflammatory, immunomodulator and antiarthritic activities. The
 CC internalising peptides are useful for facilitating the delivery, uptake
 CC and cytoplasmic and/or nuclear transport of cargo, e.g. proteins, DNA or
 CC viruses, into a target cell. The internalising peptides and peptide-cargo
 CC complexes from the present invention are also useful for inducing
 CC apoptosis in cells (e.g. arthritic cells or tumour cells), expanding a
 CC population of stem cell or differentiated cells, stimulating the
 CC differentiation of a population of stem cells, facilitating the
 CC integration of adeno-associated virus DNA into the genome of a cell,
 CC stimulating or eliciting an immune response in a subject, facilitating
 CC the delivery of immunogens (e.g. vaccines), inhibiting the inflammatory
 CC process, protecting tissue from apoptosis or necrosis during tissue
 CC isolation prior to transplantation, facilitating transfer of proteins and
 CC peptides to the lung for the treatment of cystic fibrosis or lung
 CC inflammation, or in gene therapy. The present sequence represents a
 CC peptide used in the exemplification of the present invention.
 XX
 SQ Sequence 12 AA;

Query Match 45.2%; Score 28; DB 7; Length 12;
 Best Local Similarity 44.4%; Pred. No. 3.2e+02;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3 QNFYKLPQM 11
 :||: ||::
 Db 4 KNFFWLPEL 12

RESULT 29

AAM97397

ID AAM97397 standard; peptide; 14 AA.

XX

AC AAM97397;

XX

DT 24-JAN-2002 (first entry)

XX

DE Human peptide #672 encoded by a SNP oligonucleotide.

XX

KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiopoietin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease.

XX

OS Homo sapiens.

XX

PN WO200147944-A2.

XX

PD 05-JUL-2001.

XX

PF 28-DEC-2000; 2000WO-US035498.

XX

PR 28-DEC-1999; 99US-0173419P.

PR 27-DEC-2000; 2000US-00173419.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Shimkets RA, Leach M;

XX

DR WPI; 2001-465210/50.

XX

PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.

XX

PS Disclosure; Page 3815; 4143pp; English.

XX

CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiopoietin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interferons, interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous

CC system and an infection of pathogenic organisms

XX

SQ Sequence 14 AA;

Query Match 45.2%; Score 28; DB 4; Length 14;
Best Local Similarity 71.4%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
|:| |||
Db 4 PKNSYKL 10

RESULT 30

AAR97958

ID AAR97958 standard; peptide; 15 AA.

XX

AC AAR97958;

XX

DT 16-AUG-1996 (first entry)

XX

DE Japan cedar pollen mature allergen Cry j II amino acids 436-450.

XX

KW Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;

KW Sugi pollinosis; diagnosis; treatment.

XX

OS Cryptomeria japonica.

XX

PN JP08047392-A.

XX

PD 20-FEB-1996.

XX

PF 07-NOV-1994; 94JP-00297840.

XX

PR 05-NOV-1993; 93JP-00276773.

PR 26-MAY-1994; 94JP-00134868.

XX

PA (MEIP) MEIJI MILK PROD CO LTD.

XX

DR WPI; 1996-166249/17.

XX

PT Japan cedar pollen allergen Cry j II epitope - comprises at least part of
PT specified 460 aminoacid protein.

XX

PS Disclosure; Fig 5; 17pp; Japanese.

XX

CC AAR97871-R97960 are overlapping peptides used for the epitope mapping of
CC the Japan cedar pollen allergen Cry j II. Cry j II and allergenic
CC peptides of it are useful in the diagnosis, prevention and treatment of
CC Sugi pollinosis, the allergic reaction to Japan cedar pollen. Significant
CC regions of the allergen were identified using the overlapping peptides of
CC the full epitope derived from a Cry j II antigen-specific T cell line.
CC Amino acids 66-80 (AAR97884) and 186-200 (R978908) of the full mature 460
CC amino acid allergen are the most allergenic of the 90 peptides tested

XX

SQ Sequence 15 AA;

Query Match 45.2%; Score 28; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

Qy 1 MPQNFYKLPQ 10
||| :| ||
Db 5 MPQEYY--PQ 12

RESULT 31

AAW03529

ID AAW03529 standard; peptide; 18 AA.

XX

AC AAW03529;

XX

DT 17-FEB-1997 (first entry)

XX

DE Transcriptional activation motif from human Oct-2 protein.

XX

KW Chimaeric protein; transcription activation; cleavage;

KW transcription repression; gene therapy; therapeutic protein; phenotype;

KW prophylactic protein; gene expression.

XX

OS Homo sapiens.

XX

PN WO9620951-A1.

XX

PD 11-JUL-1996.

XX

PF 29-DEC-1995; 95WO-US016982.

XX

PR 29-DEC-1994; 94US-00366083.

XX

PA (MASI) MASSACHUSETTS INST TECHNOLOGY.

XX

PI Pomerantz JL, Sharp PA, Pabo CO;

XX

DR WPI; 1996-333938/33.

XX

PT New chimaeric protein contg. two or more DNA binding domains - opt. also

PT domain that activates or represses transcription or cleaves target DNA,

PT and DNA encoding them, useful in gene therapy.

XX

PS Example 4; Page 18; 74pp; English.

XX

CC New chimaeric proteins which selectively bind DNA with Kd 10⁻⁸ or
CC better, comprise at least one composite DNA-binding region comprising a
CC continuous polypeptide chain of 2 or more component polypeptide domains,
CC at least 2 of these being mutually heterologous and additionally may also
CC comprise at least one transcription activating or repressing domain (TAD
CC or TRD), or a DNA cleaving domain (DCD), these domains being able to bind
CC to DNA sequences linked to the target DNA sequence. Genes encoding such
CC proteins are useful in gene therapy to correct/compensate for abnormal
CC gene expression, to direct expression of therapeutic/prophylactic
CC proteins or RNA and generally to modify cell phenotype. The chimaeric
CC proteins are used to express, repress or cleave the target. This
CC transcription activating domain was derived from the human Oct-2 protein

XX
SQ Sequence 18 AA;

Query Match 45.2%; Score 28; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 4.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NFYKLPQ 10
|| :|||
Db 1 NFLQLPQ 7

RESULT 32

AAY03842

ID AAY03842 standard; protein; 18 AA.

XX

AC AAY03842;

XX

DT 18-JUN-1999 (first entry)

XX

DE Activation domain of human CTF.

XX

KW Chimeric; transcription activator; DNA-binding domain; cytotoxicity;
KW proliferation; immune response; inflammatory response; clotting; p65;
KW hormonal regulation; activation domain; human.

XX

OS Homo sapiens.

XX

PN WO9910508-A1.

XX

PD 04-MAR-1999.

XX

PF 27-AUG-1997; 97WO-US015219.

XX

PR 27-AUG-1997; 97WO-US015219.

XX

PA (ARIA-) ARIAD GENE THERAPEUTICS INC.

XX

PI Sridaran N;

XX

DR WPI; 1999-190623/16.

XX

PT Nucleic acid encoding chimeric transcription activator protein - which
PT activates transcription of a gene in a cell.

XX

PS Disclosure; Page 21; 90pp; English.

XX

CC The invention relates to a nucleic acid encoding a chimeric transcription
CC activator protein which activates transcription of a gene to which the
CC chimeric transcription activator protein is targeted. The nucleic acid
CC contains at least one composite transcription activation domain
CC comprising a continuous polypeptide region containing two or more
CC component polypeptide regions, at least two of which are mutually
CC heterologous and do not occur in nature in the same gene product, and at
CC least one additional domain comprising a DNA-binding domain. The chimeric
CC proteins can be used to inhibit a transcriptional regulation protein or
CC inhibit the translation of an inhibitor of a cellular pathway. The

CC proteins can involve homing, cytotoxicity, proliferation, immune
CC response, inflammatory response, clotting or dissolving of clots,
CC hormonal regulation etc. By using the chimeric constructs, the production
CC of a specific protein is increased by stimulating expression of the
CC endogenous gene encoding the protein, with the absence of an immune
CC reaction against the protein, thereby resulting in a more efficient
CC treatment of the subject

XX

SQ Sequence 18 AA;

Query Match 45.2%; Score 28; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 4.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NFYKLPQ 10
|| :|||
Db 1 NFLQLPQ 7

RESULT 33

AAB48367

ID AAB48367 standard; peptide; 18 AA.

XX

AC AAB48367;

XX

DT 20-APR-2001 (first entry)

XX

DE Human CTF protein activation domain motif.

XX

KW Fusion protein; transcription factor; ligand binding domain; OCA-B; OAD;

KW transcription activation domain; gene therapy; therapeutic protein;

KW B cell specific transcriptional co-activator; cytokine; interleukin;

KW erythropoietin; tissue plasminogen activator; clotting factor; CTF.

XX

OS Homo sapiens.

XX

PN WO200078951-A1.

XX

PD 28-DEC-2000.

XX

PF 16-JUN-2000; 2000WO-US016620.

XX

PR 18-JUN-1999; 99US-0140289P.

XX

PA (ARIA-) ARIAD GENE THERAPEUTICS INC.

XX

PI Natesan S;

XX

DR WPI; 2001-102722/11.

XX

PT New recombinant nucleic acid encoding chimeric transcription activator,

PT useful to effect transcription of target genes in transgenic cells or

PT organisms, comprising ligand binding domain and OCA-B activation domain.

XX

PS Disclosure; Page 16; 55pp; English.

XX

CC The invention relates to a recombinant nucleic acid (I) encoding a fusion

CC protein (chimeric transcription factor) that comprises a ligand binding
 CC domain and a transcription activation domain which contains all or a part
 CC of an OCA-B (a B cell specific transcriptional co-activator) activation
 CC domain (OAD). (I) is useful for rendering a cell capable of expressing a
 CC target gene in a ligand-dependent manner. The method involves transducing
 CC a cell in vitro or in vivo, with (I) which encodes the fusion protein
 CC that stimulates, in a ligand dependent manner, the transcription of a
 CC target gene operably linked to a transcription control sequence
 CC recognized by the fusion protein. (I) and vectors, virus and cells
 CC containing (I) are useful for rendering a host organism capable of
 CC regulating expression of a target gene such as a therapeutic protein,
 CC antisense sequence or ribozyme of interest. The therapeutic proteins such
 CC as cytokines (interleukin-2, IL-4, IL-12) when expressed can involve
 CC homing, cytotoxicity, proliferation, immune response, inflammatory
 CC response, clotting or dissolving of clots or hormonal regulation etc.,
 CC and thus are useful in gene therapy techniques. The method is useful for
 CC increasing the efficacy of many gene therapy strategies by substantially
 CC elevating the expression of a therapeutic target gene allowing expression
 CC to reach therapeutically effective levels. Transcription factors encoded
 CC by (I) are also useful in the large scale production of recombinant
 CC proteins such as erythropoietin, tissue plasminogen activator, clotting
 CC factors, antibodies etc. Also, the factors encoded by (I) are useful in a
 CC range of biological experiments in which precise control over a target
 CC gene is desired. The present sequence represents an activation domain
 CC peptide motif from human CTF

XX

SQ Sequence 18 AA;

Query Match 45.2%; Score 28; DB 4; Length 18;
 Best Local Similarity 71.4%; Pred. No. 4.8e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NFYKLPQ 10
 || :|||
 Db 1 NFLQLPQ 7

RESULT 34

AAB60901

ID AAB60901 standard; peptide; 18 AA.

XX

AC AAB60901;

XX

DT 05-NOV-2001 (first entry)

XX

DE Human CTF activation domain.

XX

KW Co-activator domain; P300/CBP KIX domain; erythrocythaemia; skin disease;
 KW polycythaemia; haemoglobinopathy; cell differentiation; ulcer; cancer;
 KW neurological condition; neurodegenerative disease; immune disease;
 KW diabetes.

XX

OS Homo sapiens.

XX

PN WO200118036-A2.

XX

PD 15-MAR-2001.

XX
 PF 31-AUG-2000; 2000WO-US024010.
 XX
 PR 03-SEP-1999; 99US-0152402P.
 XX
 PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 PA (JOSL-) JOSLIN DIABETES CENT INC.
 XX
 PI Frangioni JV, Cantley LC, Montminy MR;
 XX
 DR WPI; 2001-273380/28.
 XX
 PT Identifying co-activator domain specific transcriptional activators by
 PT contacting a target domain of a selected transcription factor with a
 PT peptide display library, where the identified binding peptides are useful
 PT for reducing hyperglycemia.
 XX
 PS Disclosure; Page 42; 156pp; English.
 XX
 CC The present invention describes a method of identifying the co-activator
 CC domain of specific synthetic activators, involving contacting the target
 CC domain of a selected transcription factor with a peptide display library,
 CC and identifying those sequences which bind to the target domain. In
 CC particular, those which bind to the KIX domain of P300/CBP are useful.
 CC The peptides can be used in the treatment of diseases related to aberrant
 CC KIX-dependent gene transcription, including erythrocythaemia,
 CC polycythaemia, haemoglobinopathies, to regulate cell differentiation, to
 CC treat neurological diseases, immunological diseases, diabetes, ulcers,
 CC skin diseases and cancer, and to aid wound healing. The present sequence
 CC is a peptide described in the exemplification of the invention
 XX
 SQ Sequence 18 AA;

Query Match 45.2%; Score 28; DB 4; Length 18;
 Best Local Similarity 71.4%; Pred. No. 4.8e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NFYKLPQ 10
 || :|||
 Db 1 NFLQLPQ 7

RESULT 35

ABB07299

ID ABB07299 standard; peptide; 18 AA.

XX

AC ABB07299;

XX

DT 26-MAR-2002 (first entry)

XX

DE Chimeric transcription factor (CTF) activation domain.

XX

KW HSF; recombinant; transcription factor; ligand binding domain; LBD; TAD;

KW transcription activation domain; heat shock factor; gene therapy; human;

KW CTF.

XX

OS Homo sapiens.

XX
 PN WO200198507-A1.
 XX
 PD 27-DEC-2001.
 XX
 PF 16-JUN-2000; 2000WO-US016621.
 XX
 PR 16-JUN-2000; 2000WO-US016621.
 XX
 PA (ARIA-) ARIAD GENE THERAPEUTICS INC.
 XX
 PI Natesan S, Gilman MZ;
 XX
 DR WPI; 2002-114586/15.
 XX
 PT Novel nucleic acid encoding chimeric transcription factor having ligand
 PT binding domain, transcription activation domain that comprises heat shock
 PT factor activation domain, useful for regulating target gene expression.
 XX
 PS Disclosure; Page 16; 56pp; English.
 XX
 CC The invention relates to a recombinant nucleic acid (I) encoding a fusion
 CC protein (chimeric transcription factor) comprising ligand binding domain
 CC (LBD) and a transcription activation domain (TAD) that comprises all or a
 CC part of a heat shock factor (HSF) activation domain. (I) is useful for
 CC rendering a cell capable of expressing a target gene in a ligand-
 CC dependent manner. The method involves transducing the cell with (I) that
 CC encodes a chimeric transcription factor which stimulates, in a ligand-
 CC dependent manner, the transcription of a target gene operably linked to
 CC the transcription control sequence recognized by the transcription
 CC factor. (I), vectors, recombinant virus and cells containing (I) are
 CC useful for rendering a host organism capable of regulated expression of a
 CC target gene which involves introducing (I) into the organism. The
 CC vectors, recombinant virus and cells containing (I) are useful in gene
 CC therapy techniques for enhancing the expression of a therapeutic gene,
 CC for producing recombinant proteins, and in biological research. Non-human
 CC organisms containing one or more DNA vectors comprising (I) can be used
 CC in research to study the effect of regulated expression of target gene of
 CC possible interest and as model systems for the study of various diseases
 CC and for the evaluation of drug candidates for treating such diseases. The
 CC recombinant nucleic acids are useful for rendering a host organism
 CC capable of regulated expression of target genes that encode a therapeutic
 CC protein, antisense sequence or a ribozyme of interest. The present
 CC sequence represents the activation domain of human chimeric transcription
 CC factor (CTF)
 XX
 SQ Sequence 18 AA;

Query Match 45.2%; Score 28; DB 5; Length 18;
 Best Local Similarity 71.4%; Pred. No. 4.8e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NFYKLPQ 10
 || :|||
 Db 1 NFLQLPQ 7

RESULT 36

ABB09233

ID ABB09233 standard; peptide; 18 AA.

XX

AC ABB09233;

XX

DT 09-JUL-2002 (first entry)

XX

DE Human Oct-2 glutamine rich region 18 amino acid peptide.

XX

KW Transcription factor; protein production regulation; fusion protein;
KW regulated protein production.

XX

OS Homo sapiens.

XX

PN US2002048792-A1.

XX

PD 25-APR-2002.

XX

PF 16-JUL-2001; 2001US-00906189.

XX

PR 26-AUG-1997; 97US-00918401.

PR 27-AUG-1997; 97US-00920610.

PR 27-AUG-1997; 97WO-US015219.

PR 29-JUL-1998; 98US-00126009.

PR 26-AUG-1998; 98US-00140149.

PR 20-JAN-2000; 2000US-00488267.

XX

PA (ARIA-) ARIAD GENE THERAPEUTICS INC.

XX

PI Natesan S, Clackson TP, Pollock RM;

XX

DR WPI; 2002-382148/41.

XX

PT Producing a desired protein in a regulated manner, involves providing
PT cells containing a nucleic acid encoding a fusion protein which can bind
PT to a selected ligand.

XX

PS Disclosure; Page 8; 29pp; English.

XX

CC The present invention describes a method for producing a desired protein,
CC comprising providing cells containing a recombinant nucleic acid encoding
CC at least one fusion protein which can bind to a selected ligand, where
CC the protein contains a ligand binding domain and a DNA binding domain,
CC and in the presence of the ligand the cells express a gene operably
CC linked to regulatory DNA, exposing the cells to the ligand to produce the
CC protein, and recovering it. Also described are: (1) providing cells
CC containing recombinant nucleic acids encoding two fusion proteins which
CC self-aggregate in the absence of ligand, where: (i) the first fusion
CC protein comprises a conditional aggregation domain which binds to a
CC selected ligand and a transcription activation domain; (ii) the second
CC fusion protein comprises a conditional aggregation domain which binds to
CC a selected and a DNA binding domain; and (iii) in the absence of ligand,
CC the cells express a gene operably linked to regulatory DNA to which the
CC DNA binding domain binds; (2) expanding the cells in the presence of
CC ligand in an amount to repress the gene; (3) removing the ligand to
CC induce production of the protein; and (4) recovering the protein produced

CC from the cells. The method can be used for the regulated production of a
CC desired protein. The present sequence represents a human Oct-2 glutamine
CC rich region 18 amino acid peptide activation domain, which is given in
CC the exemplification of the present invention
XX
SQ Sequence 18 AA;

Query Match 45.2%; Score 28; DB 5; Length 18;
Best Local Similarity 71.4%; Pred. No. 4.8e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NFYKLPQ 10
|| :|||
Db 1 NFLQLPQ 7

RESULT 37

ABG76153

ID ABG76153 standard; peptide; 18 AA.

XX

AC ABG76153;

XX

DT 10-MAY-2003 (first entry)

XX

DE Human Oct-2 transcription activation domain/Glu rich region.

XX

KW Transcription activation domain; gene therapy; Oct-2;

KW tetramerisation domain; DNA binding domain; veterinary;

KW protein-protein interaction.

XX

OS Homo sapiens.

XX

PN US6479653-B1.

XX

PD 12-NOV-2002.

XX

PF 13-JUL-2000; 2000US-00615917.

XX

PR 26-AUG-1997; 97US-00918401.

PR 27-AUG-1997; 97US-00920610.

PR 29-JUL-1998; 98US-00126009.

PR 26-AUG-1998; 98US-00140149.

XX

PA (ARIA-) ARIAD GENE THERAPEUTICS INC.

XX

PI Natesan S, Gilman MZ;

XX

DR WPI; 2003-298117/29.

XX

PT New recombinant nucleic acid encoding a fusion protein comprising a
PT tetramerization or tetramerization domain, and a composite DNA binding
PT domain, useful for transducing cells for human gene therapy and
PT veterinary applications.

XX

PS Disclosure; Col 19; 47pp; English.

XX

CC The invention relates to a recombinant nucleic acid encoding a fusion

CC protein comprising a tetramerisation or tetramerisation domain, and a
 CC composite DNA binding domain and further comprises a transcription
 CC activation domain. Also included are a vector comprising the novel
 CC recombinant nucleic acid and a cell comprising the novel recombinant
 CC nucleic acid. The recombinant nucleic acids encoding the fusion proteins
 CC are useful for transducing cells to generate engineered cells which can
 CC be used in human gene therapy, veterinary applications, creation of
 CC cellular or animal models, to regulate target gene, to identify the
 CC presence of a substance which blocks the interaction of the 2 protein
 CC domains which are known to interact, and to produce a target protein in
 CC vitro. The present sequence is the human Oct-2 transcription activation
 CC domain (or glutamine rich region) which can be incorporated into a fusion
 CC protein of the invention
 XX
 SQ Sequence 18 AA;

Query Match 45.2%; Score 28; DB 6; Length 18;
 Best Local Similarity 71.4%; Pred. No. 4.8e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NFYKLPQ 10
 || :|||
 Db 1 NFLQLPQ 7

RESULT 38

ABB09499

ID ABB09499 standard; peptide; 8 AA.

XX

AC ABB09499;

XX

DT 26-JUL-2002 (first entry)

XX

DE Substance P analog used in wound healing treatment#6.

XX

KW Wound healing; insulin-like growth factor-I; tear; abrasion; skin ulcer;
 KW surgical incision; burn.

XX

OS Unidentified.

XX

PN WO200213853-A1.

XX

PD 21-FEB-2002.

XX

PF 10-AUG-2001; 2001WO-JP006933.

XX

PR 10-AUG-2000; 2000JP-00242489.

PR 28-NOV-2000; 2000JP-00361388.

XX

PA (SANT) SANTEN PHARM CO LTD.

PA (NISH/) NISHIDA T.

XX

PI Nishida T, Nakata K, Nakamura M;

XX

DR WPI; 2002-269153/31.

XX

PT Skin wound healing promoters or skin epidermal extension promoters

PT containing substance P analogs and insulin-like growth factor-I for
PT treating wounds like tear, abrasion, surgical incision, skin ulcers or
PT burns.
XX
PS Disclosure; Page 3; 20pp; Japanese.
XX
CC The invention relates to skin wound healing promoters, containing
CC substance P analogs or their pharmaceutically-acceptable salts, and
CC insulin-like growth factor-I as the active ingredient. The promoters are
CC for treating wounds like tears, abrasions, surgical incisions, or skin
CC ulcers and burns. The current sequence represents a substance P analog
CC for use in wound healing treatment
XX
SQ Sequence 8 AA;

Query Match 43.5%; Score 27; DB 5; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
|| || |
Db 1 PQQFYGL 7

RESULT 39

AAB91451

ID AAB91451 standard; peptide; 10 AA.

XX

AC AAB91451;

XX

DT 22-JUN-2001 (first entry)

XX

DE Tachykinins peptide SEQ ID NO:627.

XX

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200069900-A2.

XX

PD 23-NOV-2000.

XX

PF 17-MAY-2000; 2000WO-US013576.

XX

PR 17-MAY-1999; 99US-0134406P.

PR 10-SEP-1999; 99US-0153406P.

PR 15-OCT-1999; 99US-0159783P.

XX

PA (CONJ-) CONJUCHEM INC.

XX

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX

DR WPI; 2001-112059/12.

XX

PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure; Page 403; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 10 AA;

Query Match 43.5%; Score 27; DB 4; Length 10;
Best Local Similarity 71.4%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
|| || |
Db 4 PQQFYGL 10

RESULT 40

AAR28445

ID AAR28445 standard; peptide; 11 AA.

XX

AC AAR28445;

XX

DT 25-MAR-2003 (revised)

DT 22-MAR-1993 (first entry)

XX

DE Neurokinine 1 ligand #3.

XX

KW NK1 receptor; tumour; malignant glioma; pheochromocytoma; paraganglia;

KW small cell lung cancer; nerve regeneration; lymphoma; granuloma;

KW Crohn's disease.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 11

FT /note= "amidated"

XX

PN WO9218536-A2.

XX

PD 29-OCT-1992.
 XX
 PF 22-APR-1992; 92WO-US003307.
 XX
 PR 22-APR-1991; 91EP-00200955.
 XX
 PA (MLCW) MALLINCKRODT MEDICAL INC.
 XX
 PI Visser TJ, Lamberts SWJ, Krenning EP, Bakker WH, Hagen PM;
 XX
 DR WPI; 1992-382047/46.
 XX
 PT Detection and localisation of tissues with neurokinin-1 receptors - for
 PT detecting and treating tumours having neurokinin-1 receptors e.g.
 PT malignant glioma, small cell lung cancer etc.
 XX
 PS Disclosure; Page 4; 22pp; English.
 XX
 CC This peptide or its Tyr0 deriv. is a preferred peptide having a selective
 CC affinity to neurokinine-1 receptors which (when labelled with a
 CC radioactive isotope) can be used in imaging methods. A generic formula
 CC for preferred peptides is AAR28441. Such peptides are thus useful in
 CC diagnosis and treatment of conditions that are related to NK1 receptors
 CC and in visualising NK1 receptors on certain tissues. See AAR28442-R28446.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 43.5%; Score 27; DB 2; Length 11;
 Best Local Similarity 71.4%; Pred. No. 4.4e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
 || || |
 Db 4 PQQFYGL 10

RESULT 41

AAR42649

ID AAR42649 standard; peptide; 11 AA.

XX

AC AAR42649;

XX

DT 25-MAR-2003 (revised)

DT 19-APR-1994 (first entry)

XX

DE Neurokinin 1 receptor affinity-contg. peptide.

XX

KW Neurokinin 1; somatostatin; receptor; cytokine; growth factor; hormone;

KW intra-operativ; tumour; low energy gamma photon; radionuclide.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 11

FT /note= "the C-terminal is amidated"

XX

PN WO9318797-A1.
 XX
 PD 30-SEP-1993.
 XX
 PF 24-MAR-1993; 93WO-US002772.
 XX
 PR 25-MAR-1992; 92EP-00200848.
 XX
 PA (MLCW) MALLINCKRODT MEDICAL INC.
 XX
 PI Ensing GJ, Panek KJ, Doedens BJ;
 XX
 DR WPI; 1993-320461/40.
 XX
 PT Intra-operatively detecting and locating tumour tissues - using specific
 PT peptide(s) labelled with low energy gamma photon emitting radionuclide.
 XX
 PS Disclosure; Page 5; 31pp; English.
 XX
 CC The method of intraoperatively detecting and locating tumoral tissues
 CC makes use of peptides having selective neurokinin 1 receptor affinity
 CC (AAR42644: generic formula; AAR42646-R42650: specific examples), peptides
 CC having selective somatostatin receptor affinity (AAR42645: generic
 CC formula; AAR42651-R42660: specific examples), and peptides selected from
 CC cytokines, growth factors and hormones. (Updated on 25-MAR-2003 to
 CC correct PN field.)
 XX
 SQ Sequence 11 AA;

Query Match 43.5%; Score 27; DB 2; Length 11;
 Best Local Similarity 71.4%; Pred. No. 4.4e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
 || || |
 Db 4 PQQFYGL 10

RESULT 42

AAB91409

ID AAB91409 standard; peptide; 11 AA.

XX

AC AAB91409;

XX

DT 22-JUN-2001 (first entry)

XX

DE Tachykinins peptide SEQ ID NO:585.

XX

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200069900-A2.

XX

PD 23-NOV-2000.
 XX
 PF 17-MAY-2000; 2000WO-US013576.
 XX
 PR 17-MAY-1999; 99US-0134406P.
 PR 10-SEP-1999; 99US-0153406P.
 PR 15-OCT-1999; 99US-0159783P.
 XX
 PA (CONJ-) CONJUCHEM INC.
 XX
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 XX
 DR WPI; 2001-112059/12.
 XX
 PT Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity.
 XX
 PS Disclosure; Page 391; 733pp; English.
 XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity in
 CC vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 11 AA;

Query Match 43.5%; Score 27; DB 4; Length 11;
 Best Local Similarity 71.4%; Pred. No. 4.4e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
 || || |
 Db 4 PQQFYGL 10

RESULT 43

ABB09496

ID ABB09496 standard; peptide; 11 AA.

XX

AC ABB09496;

XX

DT 26-JUL-2002 (first entry)

XX

DE Substance P analog used in wound healing treatment#3.

XX
 KW Wound healing; insulin-like growth factor-I; tear; abrasion; skin ulcer;
 KW surgical incision; burn.
 XX
 OS Unidentified.
 XX
 PN WO200213853-A1.
 XX
 PD 21-FEB-2002.
 XX
 PF 10-AUG-2001; 2001WO-JP006933.
 XX
 PR 10-AUG-2000; 2000JP-00242489.
 PR 28-NOV-2000; 2000JP-00361388.
 XX
 PA (SANT) SANTEN PHARM CO LTD.
 PA (NISH/) NISHIDA T.
 XX
 PI Nishida T, Nakata K, Nakamura M;
 XX
 DR WPI; 2002-269153/31.
 XX
 PT Skin wound healing promoters or skin epidermal extension promoters
 PT containing substance P analogs and insulin-like growth factor-I for
 PT treating wounds like tear, abrasion, surgical incision, skin ulcers or
 PT burns.
 XX
 PS Disclosure; Page 3; 20pp; Japanese.
 XX
 CC The invention relates to skin wound healing promoters, containing
 CC substance P analogs or their pharmaceutically-acceptable salts, and
 CC insulin-like growth factor-I as the active ingredient. The promoters are
 CC for treating wounds like tears, abrasions, surgical incisions, or skin
 CC ulcers and burns. The current sequence represents a substance P analog
 CC for use in wound healing treatment
 XX
 SQ Sequence 11 AA;

Query Match 43.5%; Score 27; DB 5; Length 11;
 Best Local Similarity 71.4%; Pred. No. 4.4e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PQNFYKL 8
 || || |
 Db 4 PQQFYGL 10

RESULT 44
 AAW15279
 ID AAW15279 standard; peptide; 12 AA.
 XX
 AC AAW15279;
 XX
 DT 04-AUG-1997 (first entry)
 XX
 DE Salmonella secreted protein Ssp22 N-terminal sequence.
 XX

KW Salmonella secreted protein; Ssp22; bacterial-mediated endocytosis;
 KW diagnosis; therapy; vaccine; attenuation; virulence.
 XX
 OS Salmonella typhimurium.
 XX
 PN WO9718225-A1.
 XX
 PD 22-MAY-1997.
 XX
 PF 14-NOV-1996; 96WO-US018504.
 XX
 PR 14-NOV-1995; 95US-0006733P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PI Miller SI;
 XX
 DR WPI; 1997-289217/26.
 XX
 PT New isolated Salmonella secreted proteins and related genes - used to
 PT develop products for the detection, treatment or prevention of Salmonella
 PT infections.
 XX
 PS Disclosure; Page 57; 95pp; English.
 XX
 CC N-terminal sequences are provided (AAW15277-79) for Salmonella secreted
 CC proteins Ssp54, Ssp42 and Ssp22, respectively. Ssp proteins (see also
 CC AAW15268-71) and nucleic acids are useful for the development of products
 CC for the detection, treatment or prevention of Salmonella infections
 XX
 SQ Sequence 12 AA;

Query Match 43.5%; Score 27; DB 2; Length 12;
 Best Local Similarity 80.0%; Pred. No. 4.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQNFY 6
 ||||:
 Db 7 PQNFF 11

RESULT 45

ADC36089

ID ADC36089 standard; peptide; 12 AA.

XX

AC ADC36089;

XX

DT 18-DEC-2003 (first entry)

XX

DE Chemokine binding peptide BKT-P129.

XX

KW peptidic chemokine modulator; antiinflammatory; antiallergic;

KW immunosuppressive; antidiabetic; antirheumatic; dermatological;

KW antiarthritic; antibacterial; antipsoriatic; antiseborrheic;

KW antiarteriosclerotic; hypotensive; neuroprotective; virucide; vasotropic;

KW cytostatic; inflammation; allergy; immune response; autoimmune reaction;

KW rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis;

KW allograft rejection; diabetes; sepsis; cancer; malignant cell growth;
KW acne; infection; arthritis; colitis; psoriasis; atherosclerosis;
KW hypertension; reperfusion ischaemia.
XX
OS Synthetic.
XX
PN WO2003072599-A2.
XX
PD 04-SEP-2003.
XX
PF 27-FEB-2003; 2003WO-IL000155.
XX
PR 28-FEB-2002; 2002US-0359995P.
XX
PA (BIOK-) BIOKINE THERAPEUTICS LTD.
XX
PI Peled A, Eizenberg O, Vaizel-Ohayon D;
XX
DR WPI; 2003-671869/63.
XX
PT New peptidic chemokine modulator, useful for preparing a composition for
PT treating a disease modulated through and/or caused by binding of a
PT chemokine to a chemokine receptor, e.g., inflammation, diabetes, sepsis
PT or cancer.
XX
PS Example 1; Page 28; 43pp; English.
XX
CC The present invention describes a peptidic chemokine modulator (I) for
CC modulating a biological effect of a chemokine. (I) comprises a molecule
CC consisting of: (a) the amino acids His, Ser, Ala, Leu, Ile, Lys, Arg, Thr
CC and Pro, and features at least 2 histidines spread along the molecule,
CC where the molecule features an overall positive charge (family 1); or (b)
CC the amino acids His, Pro, Thr, Leu, Arg and Trp and features at least two
CC neighbouring histidines, where the molecule features an overall positive
CC charge (family 2). Also described: (1) a composition for treating a
CC condition involving abnormal cell migration in a subject; (2) a method
CC for treating a disease modulated through and/or caused by binding of a
CC chemokine to a chemokine receptor in a subject; (3) an antibody for
CC binding to a chemokine-binding receptor that recognises at least a
CC portion of a chemokine-binding receptor or the peptide; (4) a vaccine
CC formed with the antibody; and (5) a method for producing an antibody. (I)
CC has antiinflammatory, antiallergic, immunosuppressive, antidiabetic,
CC antirheumatic, dermatological, antiarthritic, antibacterial,
CC antipsoriatic, antiseborrheic, antiarteriosclerotic, hypotensive,
CC neuroprotective, virucide, vasotropic and cytostatic activities. The
CC peptidic chemokine modulator is useful for preparing a composition for
CC treating a disease modulated through and/or caused by binding of a
CC chemokine to a chemokine receptor, comprising inflammation (primary or
CC secondary), allergy, a non-optimal immune response, an autoimmune
CC reaction (including rheumatoid arthritis, systemic lupus erythematosus,
CC multiple sclerosis and others), allograft rejection, diabetes, sepsis,
CC cancer and any type of malignant cell growth, acne and chronic bacterial
CC and viral infections, arthritis, colitis, psoriasis, atherosclerosis,
CC hypertension or reperfusion ischaemia. The present sequence represents a
CC chemokine binding peptide, which is used in an example from the present
CC invention.
XX

SQ Sequence 12 AA;

Query Match 43.5%; Score 27; DB 7; Length 12;
Best Local Similarity 71.4%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 NFYKLPQ 10
| | |||
Db 4 NSYSLPQ 10

RESULT 46

AAR47036

ID AAR47036 standard; protein; 15 AA.

XX

AC AAR47036;

XX

DT 25-MAR-2003 (revised)

DT 16-SEP-1994 (first entry)

XX

DE Apolipoprotein B-100 position 4022-4036.

XX

KW Naturally-occurring; immunomodulatory protein; human; therapy; class I;

KW major histocompatibility complex; class II; allotype; type I diabetes;

KW autoimmune disease; rheumatoid arthritis; T-cell-mediated response;

KW multiple sclerosis; transplant rejection; vaccine; MHC.

XX

OS Homo sapiens.

XX

PN WO9404171-A1.

XX

PD 03-MAR-1994.

XX

PF 11-AUG-1993; 93WO-US007545.

XX

PR 11-AUG-1992; 92US-00925460.

PR 15-JUN-1993; 93US-00077255.

XX

PA (HARD) HARVARD COLLEGE.

XX

PI Urban RG, Chicz RM, Vignali DA, Hedley ML, Stern LJ;

PI Strominger JL;

XX

DR WPI; 1994-082825/10.

XX

PT Novel immunomodulatory peptide(s) and nucleic acids - useful for

PT treatment of autoimmune diseases, transplant rejection and for

PT vaccination.

XX

PS Disclosure; Page 49; 139pp; English.

XX

CC The sequences given in AAR49291-505 and AAR46981-7038 represent peptide
CC fragments of naturally-occurring immunomodulatory proteins. These
CC fragments are between 10-30 residues in length and bind to a human major
CC histocompatibility complex (MHC) class II allotype. These peptides may be
CC used for therapy of autoimmune diseases, such as type I diabetes,
CC rheumatoid arthritis and multiple sclerosis, and to reduce transplant

CC rejection. They may also be used for vaccination providing an exclusively
CC T-cell-mediated response, which can be class I or class-II based, or
CC both, depending on the length and character of the immunogenic peptides.
CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to
CC correct PR field.)

XX

SQ Sequence 15 AA;

Query Match 43.5%; Score 27; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 NFYKLPQ 10
||| ||
Db 2 NFYYSPQ 8

RESULT 47

AAR97957

ID AAR97957 standard; peptide; 15 AA.

XX

AC AAR97957;

XX

DT 16-AUG-1996 (first entry)

XX

DE Japan cedar pollen mature allergen Cry j II amino acids 431-445.

XX

KW Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;

KW Sugi pollinosis; diagnosis; treatment.

XX

OS Cryptomeria japonica.

XX

PN JP08047392-A.

XX

PD 20-FEB-1996.

XX

PF 07-NOV-1994; 94JP-00297840.

XX

PR 05-NOV-1993; 93JP-00276773.

PR 26-MAY-1994; 94JP-00134868.

XX

PA (MEIP) MEIJI MILK PROD CO LTD.

XX

DR WPI; 1996-166249/17.

XX

PT Japan cedar pollen allergen Cry j II epitope - comprises at least part of
PT specified 460 aminoacid protein.

XX

PS Disclosure; Fig 5; 17pp; Japanese.

XX

CC AAR97871-R97960 are overlapping peptides used for the epitope mapping of
CC the Japan cedar pollen allergen Cry j II. Cry j II and allergenic
CC peptides of it are useful in the diagnosis, prevention and treatment of
CC Sugi pollinosis, the allergic reaction to Japan cedar pollen. Significant
CC regions of the allergen were identified using the overlapping peptides of
CC the full epitope derived from a Cry j II antigen-specific T cell line.
CC Amino acids 66-80 (AAR97884) and 186-200 (R978908) of the full mature 460

CC amino acid allergen are the most allergenic of the 90 peptides tested

XX

SQ Sequence 15 AA;

Query Match 43.5%; Score 27; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPQNFY 6
||| :|
Db 10 MPQEYY 15

RESULT 48

ABR62371

ID ABR62371 standard; peptide; 17 AA.

XX

AC ABR62371;

XX

DT 22-SEP-2003 (first entry)

XX

DE Apolipoprotein J precursor, marker for Alzheimer's disease.

XX

KW Alzheimer's disease; marker; apolipoprotein J; human.

XX

OS Homo sapiens.

XX

PN WO2003046571-A2.

XX

PD 05-JUN-2003.

XX

PF 31-OCT-2002; 2002WO-CA001654.

XX

PR 23-NOV-2001; 2001US-00993364.

XX

PA (SYNX-) SYN.X PHARMA INC.

XX

PI Jackowski G, Marshall J;

XX

DR WPI; 2003-505226/47.

XX

PT New HP and apolipoprotein biopolymer markers, or their analyte, useful in
PT indicating at least one particular disease state that is particularly
PT predictive of Alzheimer's disease.

XX

PS Claim 1; Page 45; 45pp; English.

XX

CC The present sequence is that of an apolipoprotein J precursor peptide,
CC characterised as a specific marker for Alzheimer's disease using the
CC method of the invention. This relates to the use of mass spectrometry and
CC time-of-flight detection procedures to elucidate biopolymer markers
CC indicative or predictive of a particular disease state, especially
CC markers whose up-regulation, down-regulation or relative presence in
CC disease versus normal states has been determined to be useful in disease
CC state assessment and therapeutic target recognition, development and
CC validation. Methods and kits are claimed for diagnosis, risk assessment
CC and identification of therapeutic avenues. A process for regulating a

CC disease state by controlling the presence of absence of a biopolymer,
CC such as a biopolymer having the present sequence, is also claimed
XX
SQ Sequence 17 AA;

Query Match 43.5%; Score 27; DB 7; Length 17;
Best Local Similarity 62.5%; Pred. No. 6.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PQNFYKLP 9
||: | ||
Db 3 PQDTYYLP 10

RESULT 49

ABG68026

ID ABG68026 standard; peptide; 9 AA.

XX

AC ABG68026;

XX

DT 07-OCT-2002 (first entry)

XX

DE Human ADPI tryptic digest peptide #735.

XX

KW Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;

KW Alzheimer's disease-associated feature; neuroprotective;

KW Alzheimer's disease-associated protein isoform; nootropic;

KW ADPI tryptic digest peptide.

XX

OS Homo sapiens.

XX

PN WO200246767-A2.

XX

PD 13-JUN-2002.

XX

PF 29-NOV-2001; 2001WO-GB005289.

XX

PR 08-DEC-2000; 2000US-0254431P.

XX

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX

PI Herath HMAc, Parekh RB, Rohlf C;

XX

DR WPI; 2002-508575/54.

XX

PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,
PT comprises detecting Alzheimer disease-associated features or Alzheimer
PT disease-associated protein isoforms in brain tissue from the subject.

XX

PS Claim 7; Page 68; 427pp; English.

XX

CC The present invention relates to methods and compositions for the
CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in a
CC subject. The method comprises analysing a sample of brain tissue from a
CC subject by 2D electrophoresis to generate a 2D array of Alzheimer's
CC disease-associated features (ADFs), whose relative abundance correlates
CC with the presence, absence, stage or severity of AD and comparing the

CC abundance of each feature with the abundance of that chosen feature in
CC brain tissue from persons free from AD. The invention also describes
CC Alzheimer's disease-associated protein isoforms (ADPIs) detectable in
CC brain tissue. The methods and compositions of the invention are useful
CC for the screening, diagnosis or prognosis of AD in a subject, for
CC determining the stage or severity of AD in a subject, for identifying a
CC subject at risk of developing AD, or for monitoring the effect of therapy
CC administered to a subject having AD. Antibodies capable of binding to
CC ADPIs are useful for treating or preventing AD, and for determining the
CC efficacy of a given treatment regime. An agent that modulates the
CC activity of ADPI is useful in the manufacture of a medicament for the
CC treatment or prevention of AD in a subject. ABG67292-ABG68038 represent
CC human ADPI tryptic digest peptides

XX

SQ Sequence 9 AA;

Query Match 41.9%; Score 26; DB 5; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8

|:|:|

Db 2 PENFFLL 8

RESULT 50

ADA24181

ID ADA24181 standard; peptide; 9 AA.

XX

AC ADA24181;

XX

DT 20-NOV-2003 (first entry)

XX

DE Alzheimer's disease-associated protein isoform tryptic peptide #790.

XX

KW human; Alzheimer's disease; vascular dementia; Lewy body dementia;

KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;

KW Alzheimer's disease-associated protein isoform; ADPI.

XX

OS Homo sapiens.

XX

PN US2003064411-A1.

XX

PD 03-APR-2003.

XX

PF 10-DEC-2001; 2001US-00014340.

XX

PR 08-DEC-2000; 2000US-0254431P.

XX

PA (HERA/) HERATH H M A C.

PA (PARE/) PAREKH R B.

PA (ROHL/) ROHLFF C.

XX

PI Herath HMAc, Parekh RB, Rohlff C;

XX

DR WPI; 2003-540784/51.

XX

PT Screening, diagnosis or prognosis of Alzheimer's disease in subject,
PT involves analyzing test sample of brain tissue from subject, and
PT comparing feature in test sample with that of person(s) free from
PT Alzheimer's disease.

XX

PS Disclosure; SEQ ID NO 790; 115pp; English.

XX

CC The invention relates to a method of screening or diagnosing Alzheimer's
CC disease in a subject. The method is useful for screening, diagnosis or
CC prognosis of Alzheimer's disease in a subject for determining the stage
CC of severity of Alzheimer's disease in a subject, for identifying a
CC subject at risk of developing Alzheimer's disease, or for monitoring the
CC effect of therapy administered to a subject having Alzheimer's disease.
CC The method is also useful in treating vascular dementia, Lewy body
CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or
CC depression. The inventive method identifies sensitive and specific
CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.
CC It provides therapeutic agents for Alzheimer's disease that works
CC quickly, potently, specifically with fewer side effects. The present
CC sequence represents the amino acid sequence of a Alzheimer's disease-
CC associated protein isoform tryptic peptide.

XX

SQ Sequence 9 AA;

Query Match 41.9%; Score 26; DB 6; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.4e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
|:|:|:
Db 2 PENFFLL 8

Search completed: July 4, 2004, 04:40:50
Job time : 29.7761 secs

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:37:26 ; Search time 6.89552 Seconds
(without alignments)
82.356 Million cell updates/sec

Title: US-09-641-802-6
Perfect score: 62
Sequence: 1 MPQNFYKLPQM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 121837

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	62	100.0	11	4	US-09-641-803-6	Sequence 6, Appli
2	30	48.4	8	1	US-08-014-426-53	Sequence 53, Appl
3	30	48.4	8	1	US-08-014-426-60	Sequence 60, Appl
4	30	48.4	8	5	PCT-US94-01319-53	Sequence 53, Appl
5	30	48.4	8	5	PCT-US94-01319-60	Sequence 60, Appl
6	30	48.4	11	2	US-07-737-371E-64	Sequence 64, Appl
7	29	46.8	15	4	US-09-000-003A-11	Sequence 11, Appl
8	28	45.2	18	3	US-08-920-610-4	Sequence 4, Appli
9	28	45.2	18	3	US-09-140-149-2	Sequence 2, Appli
10	28	45.2	18	4	US-08-672-213-4	Sequence 4, Appli
11	28	45.2	18	4	US-08-973-131-31	Sequence 31, Appl

12	28	45.2	18	4	US-09-615-917-2	Sequence 2, Appli
13	27	43.5	15	2	US-08-480-190-271	Sequence 271, App
14	27	43.5	15	2	US-08-488-379-271	Sequence 271, App
15	27	43.5	15	4	US-08-475-399A-271	Sequence 271, App
16	27	43.5	15	5	PCT-US93-07545-271	Sequence 271, App
17	26	41.9	10	2	US-08-934-222-93	Sequence 93, Appl
18	26	41.9	10	2	US-08-933-402-93	Sequence 93, Appl
19	26	41.9	10	2	US-09-207-621-93	Sequence 93, Appl
20	26	41.9	10	2	US-08-532-818-93	Sequence 93, Appl
21	26	41.9	10	3	US-09-231-797-93	Sequence 93, Appl
22	26	41.9	10	3	US-08-934-224-93	Sequence 93, Appl
23	26	41.9	10	3	US-08-933-843-93	Sequence 93, Appl
24	26	41.9	10	3	US-08-934-223-93	Sequence 93, Appl
25	26	41.9	10	3	US-09-413-492-93	Sequence 93, Appl
26	26	41.9	11	2	US-08-704-655-18	Sequence 18, Appl
27	26	41.9	16	3	US-08-462-436-22	Sequence 22, Appl
28	26	41.9	16	3	US-08-465-275-22	Sequence 22, Appl
29	26	41.9	16	4	US-08-640-877-22	Sequence 22, Appl
30	26	41.9	16	4	US-09-799-576A-22	Sequence 22, Appl
31	26	41.9	16	4	US-09-799-540-22	Sequence 22, Appl
32	25	40.3	8	2	US-08-765-061-9	Sequence 9, Appli
33	25	40.3	8	4	US-09-514-739-2	Sequence 2, Appli
34	25	40.3	10	1	US-07-954-213-4	Sequence 4, Appli
35	25	40.3	10	2	US-08-765-061-7	Sequence 7, Appli
36	25	40.3	11	2	US-07-737-371E-39	Sequence 39, Appl
37	25	40.3	11	2	US-07-737-371E-40	Sequence 40, Appl
38	25	40.3	11	4	US-09-579-883A-12	Sequence 12, Appl
39	25	40.3	12	1	US-08-275-983B-17	Sequence 17, Appl
40	25	40.3	12	4	US-08-794-002-10	Sequence 10, Appl
41	25	40.3	12	4	US-08-854-039B-10	Sequence 10, Appl
42	25	40.3	12	4	US-08-765-702B-10	Sequence 10, Appl
43	25	40.3	15	2	US-08-637-418-9	Sequence 9, Appli
44	25	40.3	15	2	US-08-637-418-10	Sequence 10, Appl
45	25	40.3	16	1	US-07-954-213-12	Sequence 12, Appl
46	25	40.3	16	3	US-07-861-458C-134	Sequence 134, App
47	24	38.7	7	2	US-08-968-676-69	Sequence 69, Appl
48	24	38.7	8	4	US-09-266-764-26	Sequence 26, Appl
49	24	38.7	9	1	US-08-024-253-18	Sequence 18, Appl
50	24	38.7	9	2	US-08-629-291A-27	Sequence 27, Appl
51	24	38.7	9	2	US-08-658-335B-27	Sequence 27, Appl
52	24	38.7	9	3	US-08-159-339A-367	Sequence 367, App
53	24	38.7	9	3	US-07-987-264-6	Sequence 6, Appli
54	24	38.7	9	4	US-09-492-543-73	Sequence 73, Appl
55	24	38.7	9	4	US-09-492-543-101	Sequence 101, App
56	24	38.7	9	4	US-09-406-640-27	Sequence 27, Appl
57	24	38.7	11	2	US-07-737-371E-20	Sequence 20, Appl
58	24	38.7	11	2	US-07-737-371E-21	Sequence 21, Appl
59	24	38.7	11	2	US-07-737-371E-22	Sequence 22, Appl
60	24	38.7	11	2	US-07-737-371E-23	Sequence 23, Appl
61	24	38.7	11	2	US-07-737-371E-24	Sequence 24, Appl
62	24	38.7	11	2	US-07-737-371E-27	Sequence 27, Appl
63	24	38.7	11	2	US-07-737-371E-37	Sequence 37, Appl
64	24	38.7	11	2	US-07-737-371E-55	Sequence 55, Appl
65	24	38.7	11	2	US-07-737-371E-65	Sequence 65, Appl
66	24	38.7	11	6	5441935-8	Patent No. 5441935
67	24	38.7	12	2	US-08-811-492-145	Sequence 145, App
68	24	38.7	12	2	US-08-811-492-147	Sequence 147, App

69	24	38.7	15	2	US-08-637-418-19	Sequence 19, Appl
70	24	38.7	15	2	US-08-637-418-20	Sequence 20, Appl
71	24	38.7	15	2	US-08-101-624-19	Sequence 19, Appl
72	24	38.7	15	3	US-08-596-257A-10	Sequence 10, Appl
73	24	38.7	15	3	US-08-479-744A-19	Sequence 19, Appl
74	24	38.7	15	3	US-08-860-339-10	Sequence 10, Appl
75	24	38.7	15	3	US-08-280-757B-19	Sequence 19, Appl
76	24	38.7	15	4	US-09-227-357-539	Sequence 539, App
77	24	38.7	15	4	US-09-370-644B-10	Sequence 10, Appl
78	24	38.7	15	4	US-09-425-762-19	Sequence 19, Appl
79	24	38.7	15	4	US-09-573-629-10	Sequence 10, Appl
80	24	38.7	16	1	US-08-477-509B-17	Sequence 17, Appl
81	24	38.7	16	3	US-08-482-085B-17	Sequence 17, Appl
82	24	38.7	16	3	US-07-861-458C-135	Sequence 135, App
83	24	38.7	16	4	US-09-444-791A-17	Sequence 17, Appl
84	24	38.7	17	3	US-08-691-563C-42	Sequence 42, Appl
85	24	38.7	17	4	US-09-374-766-42	Sequence 42, Appl
86	24	38.7	17	4	US-08-979-847B-38	Sequence 38, Appl
87	23	37.1	7	1	US-07-841-997A-19	Sequence 19, Appl
88	23	37.1	7	1	US-08-290-301-19	Sequence 19, Appl
89	23	37.1	7	4	US-09-013-598-19	Sequence 19, Appl
90	23	37.1	8	2	US-07-737-371E-10	Sequence 10, Appl
91	23	37.1	8	4	US-09-601-729-275	Sequence 275, App
92	23	37.1	8	6	5514646-22	Patent No. 5514646
93	23	37.1	9	1	US-08-787-547-101	Sequence 101, App
94	23	37.1	9	1	US-08-290-301-80	Sequence 80, Appl
95	23	37.1	9	2	US-07-737-371E-60	Sequence 60, Appl
96	23	37.1	9	3	US-08-505-250-29	Sequence 29, Appl
97	23	37.1	9	4	US-09-492-543-149	Sequence 149, App
98	23	37.1	9	4	US-09-492-543-159	Sequence 159, App
99	23	37.1	9	4	US-08-505-250-29	Sequence 29, Appl
100	23	37.1	9	4	US-09-013-598-80	Sequence 80, Appl

ALIGNMENTS

RESULT 1

US-09-641-803-6

; Sequence 6, Application US/09641803

; Patent No. 6500798

; GENERAL INFORMATION:

; APPLICANT: STANTON, G. John

; APPLICANT: HUGHES, Thomas K.

; APPLICANT: BOLDOGH, Istvan

; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND

; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS

; FILE REFERENCE: 265.00220101

; CURRENT APPLICATION NUMBER: US/09/641,803

; CURRENT FILING DATE: 2000-08-17

; PRIOR APPLICATION NUMBER: 60/149,310

; PRIOR FILING DATE: 1999-08-17

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-803-6

Query Match 100.0%; Score 62; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFYKLPQM 11
|||||||
Db 1 MPQNFYKLPQM 11

RESULT 2

US-08-014-426-53

; Sequence 53, Application US/08014426
; Patent No. 5512435

; GENERAL INFORMATION:

; APPLICANT: Renschler, Markus F.
; APPLICANT: Levy, Ronald
; APPLICANT: Bhatt, Ramesh
; APPLICANT: Dower, William
; TITLE OF INVENTION: RECEPTOR-BINDING ANTIPROLIFERATIVE
; TITLE OF INVENTION: PEPTIDES
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/014,426
; FILING DATE: 05-FEB-1993
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, Willaim M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 5490A-204

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 53:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO
US-08-014-426-53

Query Match 48.4%; Score 30; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFYK 7
||::||:
Db 1 MPEDFYR 7

RESULT 3

US-08-014-426-60

; Sequence 60, Application US/08014426

; Patent No. 5512435

; GENERAL INFORMATION:

; APPLICANT: Renschler, Markus F.

; APPLICANT: Levy, Ronald

; APPLICANT: Bhatt, Ramesh

; APPLICANT: Dower, William

; TITLE OF INVENTION: RECEPTOR-BINDING ANTIPROLIFERATIVE

; TITLE OF INVENTION: PEPTIDES

; NUMBER OF SEQUENCES: 65

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/014,426

; FILING DATE: 05-FEB-1993

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, Willaim M

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 5490A-204

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 60:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

US-08-014-426-60

Query Match 48.4%; Score 30; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFYK 7
||::||:
Db 1 MPEDFYR 7

RESULT 4

PCT-US94-01319-53

; Sequence 53, Application PC/TUS9401319

; GENERAL INFORMATION:

; APPLICANT: Renschler, Markus F.

; APPLICANT: Levy, Ronald

; APPLICANT: Bhatt, Ramesh

; APPLICANT: Dower, William

; TITLE OF INVENTION: RECEPTOR-BINDING ANTIPROLIFERATIVE

; TITLE OF INVENTION: PEPTIDES

; NUMBER OF SEQUENCES: 65

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/01319

; FILING DATE: 04-FEB-1994

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/014,426

; FILING DATE: 05-FEB-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, Willaim M

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 5490A-204

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 53:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

PCT-US94-01319-53

Query Match 48.4%; Score 30; DB 5; Length 8;

Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFYK 7
| | : | | :
Db 1 MPEDFYR 7

RESULT 5

PCT-US94-01319-60

; Sequence 60, Application PC/TUS9401319

; GENERAL INFORMATION:

; APPLICANT: Renschler, Markus F.

; APPLICANT: Levy, Ronald

; APPLICANT: Bhatt, Ramesh

; APPLICANT: Dower, William

; TITLE OF INVENTION: RECEPTOR-BINDING ANTIPROLIFERATIVE

; TITLE OF INVENTION: PEPTIDES

; NUMBER OF SEQUENCES: 65

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend Khourie and Crew

; STREET: 379 Lytton Avenue

; CITY: Palo Alto

; STATE: California

; COUNTRY: US

; ZIP: 94301

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/01319

; FILING DATE: 04-FEB-1994

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/014,426

; FILING DATE: 05-FEB-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Smith, Willaim M

; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 5490A-204

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 326-2400

; TELEFAX: (415) 326-2422

; INFORMATION FOR SEQ ID NO: 60:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

PCT-US94-01319-60

Query Match 48.4%; Score 30; DB 5; Length 8;
Best Local Similarity 57.1%; Pred. No. 3e+05;

Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFYK 7
||::||:
Db 1 MPEDFYR 7

RESULT 6

US-07-737-371E-64

; Sequence 64, Application US/07737371E

; Patent No. 5876948

; GENERAL INFORMATION:

; APPLICANT: Yankner, Bruce A.

; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY

; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)

; NUMBER OF SEQUENCES: 77

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: US

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: Windows95

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/737,371E

; FILING DATE: 29-JUL-1991

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/559,172

; FILING DATE: 27-JUL-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Freeman, John W.

; REGISTRATION NUMBER: 29,066

; REFERENCE/DOCKET NUMBER: 00108/028002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-542-5070

; TELEFAX: 617-542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 64:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-07-737-371E-64

Query Match 48.4%; Score 30; DB 2; Length 11;

Best Local Similarity 62.5%; Pred. No. 21;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKLP 9
|| |: ||

RESULT 7

US-09-000-003A-11

; Sequence 11, Application US/09000003A

; Patent No. 6652850

; GENERAL INFORMATION:

; APPLICANT: Philip, Ramila

; Lebkowski, Jane S.

; TITLE OF INVENTION: ADENO-ASSOCIATED VIRAL LIPOSOMES AND

; THEIR USE IN TRANSFECTING DENDRITIC CELLS TO

STIMULATE

; SPECIFIC IMMUNITY

; NUMBER OF SEQUENCES: 30

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Alexis Barron, Esq.

; STREET: Suite 2600 Aramark Tower, 1101 Market Street

; CITY: Philadelphia

; STATE: PA

; COUNTRY: United States of America

; ZIP: 19107

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/000,003A

; FILING DATE: 15-Jun-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/12012

; FILING DATE: 19-JUL-1996

; APPLICATION NUMBER: US 60/001,312

; FILING DATE: 21-JUL-1995

; APPLICATION NUMBER: US 60/007,184

; FILING DATE: 01-NOV-1995

; APPLICATION NUMBER: US 08/566,286

; FILING DATE: 01-DEC-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Barron, Alexis

; REGISTRATION NUMBER: 22,702

; REFERENCE/DOCKET NUMBER: 20,846-K USA

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 923-4466

; TELEFAX: (215) 923-2189

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 15 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: N-terminal

; SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-09-000-003A-11

Query Match 46.8%; Score 29; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 45;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PQNFYKLPQM 11
| ||:| |
Db 4 PTVFYNI PPM 13

RESULT 8

US-08-920-610-4

; Sequence 4, Application US/08920610

; Patent No. 6015709

; GENERAL INFORMATION:

; APPLICANT: Natesan, Sridaran

; TITLE OF INVENTION: TRANSCRIPTIONAL ACTIVATORS, AND

; TITLE OF INVENTION: COMPOSITIONS AND USES RELATED THERETO

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HOAG & ELIOT LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109-2170

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/920,610

; FILING DATE: 27-AUG-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: APV-006.02

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-832-1000

; TELEFAX: 617-832-7000

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 18 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-920-610-4

Query Match 45.2%; Score 28; DB 3; Length 18;
Best Local Similarity 71.4%; Pred. No. 82;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NFYKLPQ 10
||:|||
Db 1 NFLQLPQ 7

RESULT 9

US-09-140-149-2

; Sequence 2, Application US/09140149
 ; Patent No. 6117680
 ; GENERAL INFORMATION:
 ; APPLICANT: Natesan, Sridaran
 ; APPLICANT: Gilman, Michael Z
 ; TITLE OF INVENTION: No. 6117680el Compositions and Methods for Regulation of
 ; TITLE OF INVENTION: Transcription
 ; FILE REFERENCE: 363C
 ; CURRENT APPLICATION NUMBER: US/09/140,149
 ; CURRENT FILING DATE: 1998-08-26
 ; EARLIER APPLICATION NUMBER: 08/918,401
 ; EARLIER FILING DATE: 1997-08-26
 ; EARLIER APPLICATION NUMBER: 08/920,610
 ; EARLIER FILING DATE: 1997-08-27
 ; EARLIER APPLICATION NUMBER: 09/126,009
 ; EARLIER FILING DATE: 1998-07-29
 ; EARLIER APPLICATION NUMBER: PCT/US97/15219
 ; EARLIER FILING DATE: 1997-08-27
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-140-149-2

Query Match 45.2%; Score 28; DB 3; Length 18;
 Best Local Similarity 71.4%; Pred. No. 82;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NFYKLPQ 10
 || :|||
 Db 1 NFLQLPQ 7

RESULT 10

US-08-672-213-4

; Sequence 4, Application US/08672213
 ; Patent No. 6306649
 ; GENERAL INFORMATION:
 ; APPLICANT: GILMAN, Michael Z.
 ; APPLICANT: NATESAN, Sridaran
 ; TITLE OF INVENTION: USE OF HETEROLOGOUS TRANSCRIPTION
 ; TITLE OF INVENTION: FACTORS IN GENE THERAPY
 ; NUMBER OF SEQUENCES: 72
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ARIAD Gene Therapeutics, Inc.
 ; STREET: 26 Landsdowne Street
 ; CITY: Cambridge
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02139-4234
 ; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,213
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,553
; FILING DATE: 27-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,614
; FILING DATE: 29-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BERSTEIN, David L.
; REGISTRATION NUMBER: 31,235
; REFERENCE/DOCKET NUMBER: ARIAD 346B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-494-0400
; TELEFAX: 617-494-0208
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-213-4

```

```

Query Match          45.2%; Score 28; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 82;
Matches      5; Conservative      1; Mismatches      1; Indels      0; Gaps      0;

```

```

Qy      4 NFYKLPQ 10
        || :|||
Db      1 NFLQLPQ 7

```

```

RESULT 11
US-08-973-131-31
; Sequence 31, Application US/08973131
; Patent No. 6326166
; GENERAL INFORMATION:
; APPLICANT: Pomerantz, Joel L.
; APPLICANT: Sharp, Phillip A.
; APPLICANT: Pabo, Carl O.
; TITLE OF INVENTION: Chimeric DNA-binding proteins
; FILE REFERENCE: APV-022.02
; CURRENT APPLICATION NUMBER: US/08/973,131
; CURRENT FILING DATE: 1998-03-16
; EARLIER APPLICATION NUMBER: PCT/US95/16982
; EARLIER FILING DATE: 1995-12-29
; EARLIER APPLICATION NUMBER: 08/366,083
; EARLIER FILING DATE: 1994-12-29
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0

```

; SEQ ID NO 31
; LENGTH: 18
; TYPE: PRT
; ORGANISM: human
US-08-973-131-31

Query Match 45.2%; Score 28; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 82;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NFYKLPQ 10
|| :|||
Db 1 NFLQLPQ 7

RESULT 12

US-09-615-917-2

; Sequence 2, Application US/09615917
; Patent No. 6479653
; GENERAL INFORMATION:
; APPLICANT: Natesan, Sridaran
; APPLICANT: Gilman, Michael Z
; TITLE OF INVENTION: No. 6479653el Compositions and Methods for Regulation of
; TITLE OF INVENTION: Transcription
; FILE REFERENCE: 363C continuation
; CURRENT APPLICATION NUMBER: US/09/615,917
; CURRENT FILING DATE: 2000-07-13
; PRIOR APPLICATION NUMBER: 08/918,401
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 08/920,610
; PRIOR FILING DATE: 1997-08-27
; PRIOR APPLICATION NUMBER: 09/126,009
; PRIOR FILING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: 09/140,149
; PRIOR FILING DATE: 1998-08-26
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-615-917-2

Query Match 45.2%; Score 28; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 82;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NFYKLPQ 10
|| :|||
Db 1 NFLQLPQ 7

RESULT 13

US-08-480-190-271

; Sequence 271, Application US/08480190
; Patent No. 5827516
; GENERAL INFORMATION:

```

; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 271:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-480-190-271

```

```

Query Match          43.5%; Score 27; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches    5; Conservative    0; Mismatches    2; Indels    0; Gaps    0;

```

```

Qy      4 NFYKLPQ 10
      |||  ||
Db      2 NFYYSPQ 8

```

```

RESULT 14
US-08-488-379-271
; Sequence 271, Application US/08488379

```

```

; Patent No. 5880103
; GENERAL INFORMATION:
;   APPLICANT: Robert G. Urban
;   APPLICANT: Roman M. Chicz
;   APPLICANT: Dario A. A. Vignali
;   APPLICANT: Mary L. Hedley
;   APPLICANT: Lawrence J. Stern
;   APPLICANT: Jack L. Strominger
;   TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
;   NUMBER OF SEQUENCES: 274
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Fish & Richardson
;     STREET: 225 Franklin Street
;     CITY: Boston
;     STATE: Massachusetts
;     COUNTRY: U.S.A.
;     ZIP: 02110-2804
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;     COMPUTER: IBM PS/2 Model 50Z or 55SX
;     OPERATING SYSTEM: MS-DOS (Version 5.0)
;     SOFTWARE: WordPerfect (Version 5.1)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/488,379
;     FILING DATE:
;     CLASSIFICATION: 514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/077,255
;     FILING DATE: June 15, 1993
;     APPLICATION NUMBER: 07/925,460
;     FILING DATE: August 11, 1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Clark, Paul T.
;     REGISTRATION NUMBER: 30,162
;     REFERENCE/DOCKET NUMBER: 00246/168001
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (617) 542-5070
;     TELEFAX: (617) 542-8906
;     TELEX: 200154
;   INFORMATION FOR SEQ ID NO: 271:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 15
;       TYPE: amino acid
;       STRANDEDNESS:
;       TOPOLOGY: linear
US-08-488-379-271

```

```

Query Match          43.5%; Score 27; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches      5; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

```

```

Qy      4 NFYKLPQ 10
        |||  ||
Db      2 NFYYSPQ 8

```

RESULT 15

US-08-475-399A-271
; Sequence 271, Application US/08475399A
; Patent No. 6509033
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; APPLICANT: Vignali, Dario A.A.
; APPLICANT: Hedley, Mary L.
; APPLICANT: Stern, Lawrence J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 276
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,399A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: 15-JUN-1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: 11-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00246/168003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-507
; TELEFAX: 617/542-890
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 271:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-475-399A-271

Query Match 43.5%; Score 27; DB 4; Length 15;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 NFYKLPQ 10
||| ||
Db 2 NFYYSPQ 8

RESULT 16

PCT-US93-07545-271
; Sequence 271, Application PC/TUS9307545
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07545
; FILING DATE: 19930811
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 271:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
PCT-US93-07545-271

Query Match 43.5%; Score 27; DB 5; Length 15;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 NFYKLPQ 10
||| ||
Db 2 NFYYSPQ 8

RESULT 17
US-08-934-222-93

```

; Sequence 93, Application US/08934222
; Patent No. 5928896
; GENERAL INFORMATION:
;   APPLICANT: EVANS, Herbert J.
;   APPLICANT: KINI, R. Manjunatha
;   TITLE OF INVENTION: Polypeptides That Include Conformation-
;   TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction
;   TITLE OF INVENTION: Site
;   NUMBER OF SEQUENCES: 153
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Foley & Lardner
;     STREET: Suite 500, 3000 K Street NW
;     CITY: Washington
;     STATE: DC
;     COUNTRY: USA
;     ZIP: 20007
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/934,222
;     FILING DATE: 19-SEPT-1997
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: 08/532,818
;     FILING DATE: 03-MAY-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: U.S. 08/143,364
;     FILING DATE: 29-OCT-1993
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: U.S. 08/051,741
;     FILING DATE: 23-APR-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Isacson, John P.
;     REGISTRATION NUMBER: 33,751
;     REFERENCE/DOCKET NUMBER: 040433/0148
;   INFORMATION FOR SEQ ID NO: 93:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 10 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
US-08-934-222-93

```

```

Query Match          41.9%; Score 26; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches    5; Conservative    0; Mismatches    3; Indels    0; Gaps    0;

```

```

Qy      2 PQNFYKLP 9
        | | |||
Db      2 PNNLDKLP 9

```

RESULT 18

US-08-933-402-93

; Sequence 93, Application US/08933402

; Patent No. 5948887
; GENERAL INFORMATION:
; APPLICANT: EVANS, Herbert J.
; APPLICANT: KINI, R. Manjunatha
; TITLE OF INVENTION: Polypeptides That Include Conformation-
; TITLE OF INVENTION: Constraining Groups Which Flank A Protein-Protein
Interaction

; TITLE OF INVENTION: Site
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20007
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,402
; FILING DATE: 19-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/532,818
; FILING DATE: 03-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/143,364
; FILING DATE: 29-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. 08/051,741
; FILING DATE: 23-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Isacson, John P.
; REGISTRATION NUMBER: 33,751
; REFERENCE/DOCKET NUMBER: 040433/0148
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-933-402-93

Query Match 41.9%; Score 26; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PQNFYKLP 9
| | |||
Db 2 PNNLDKLP 9

RESULT 19
US-09-207-621-93
; Sequence 93, Application US/09207621
; Patent No. 5952465

```

; GENERAL INFORMATION:
;   APPLICANT:  EVANS, Herbert J.
;   APPLICANT:  KINI, R. Manjunatha
;   TITLE OF INVENTION:  Polypeptides That Include Conformation-
;   TITLE OF INVENTION:  Constraining Groups Which Flank A Protein-Protein
Interaction Site
;   NUMBER OF SEQUENCES:  153
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Foley & Lardner
;     STREET:    Suite 500, 3000 K Street NW
;     CITY:      Washington
;     STATE:     DC
;     COUNTRY:   USA
;     ZIP:       20007
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:     IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:     PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/207,621
;     FILING DATE:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/532,818
;     FILING DATE:        03-MAY-1996
;     APPLICATION NUMBER:  PCT/US94/04294
;     FILING DATE:        21-APR-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  U.S. 08/143,364
;     FILING DATE:        29-OCT-1993
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  U.S. 08/051,741
;     FILING DATE:        23-APR-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Isacson, John P.
;     REGISTRATION NUMBER:  33,751
;     REFERENCE/DOCKET NUMBER:  040433/0148
;   INFORMATION FOR SEQ ID NO:  93:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 amino acids
;       TYPE:    amino acid
;       TOPOLOGY:  linear
US-09-207-621-93

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```

Query Match          41.9%;  Score 26;  DB 2;  Length 10;
Best Local Similarity 62.5%;  Pred. No. 1e+02;
Matches      5;  Conservative      0;  Mismatches      3;  Indels      0;  Gaps      0;

```

```

Qy      2 PQNFYKLP 9
        | |  |||
Db      2 PNNLDKLP 9

```

```

RESULT 20
US-08-532-818-93
; Sequence 93, Application US/08532818
; Patent No. 5965698

```

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; GENERAL INFORMATION:
;   APPLICANT:  EVANS, Herbert J.
;   APPLICANT:  KINI, R. Manjunatha
;   TITLE OF INVENTION:  Polypeptides That Include Conformation-
;   TITLE OF INVENTION:  Constraining Groups Which Flank A Protein-Protein
Interaction
;   TITLE OF INVENTION:  Site
;   NUMBER OF SEQUENCES:  153
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Foley & Lardner
;     STREET:    Suite 500, 3000 K Street NW
;     CITY:      Washington
;     STATE:     DC
;     COUNTRY:   USA
;     ZIP:       20007
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:     IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:     PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/532,818
;     FILING DATE:       03-MAY-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/US94/04294
;     FILING DATE:       21-APR-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  U.S. 08/143,364
;     FILING DATE:       29-OCT-1993
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  U.S. 08/051,741
;     FILING DATE:       23-APR-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Isacson, John P.
;     REGISTRATION NUMBER:  33,751
;     REFERENCE/DOCKET NUMBER:  040433/0148
;   INFORMATION FOR SEQ ID NO: 93:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 amino acids
;       TYPE:    amino acid
;       TOPOLOGY:  linear
US-08-532-818-93

```

```

Query Match          41.9%;  Score 26;  DB 2;  Length 10;
Best Local Similarity 62.5%;  Pred. No. 1e+02;
Matches      5;  Conservative      0;  Mismatches      3;  Indels      0;  Gaps      0;

```

```

Qy      2 PQNFYKLP 9
        | |  |||
Db      2 PNNLDKLP 9

```

```

RESULT 21
US-09-231-797-93
; Sequence 93, Application US/09231797
; Patent No. 6084066
; GENERAL INFORMATION:

```

```

;   APPLICANT:  EVANS, Herbert J.
;   APPLICANT:  KINI, R. Manjunatha
;   TITLE OF INVENTION:  Polypeptides That Include Conformation-
;   TITLE OF INVENTION:  Constraining Groups Which Flank A Proten-Protein
Interaction Sit
;   NUMBER OF SEQUENCES:  153
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Foley & Lardner
;       STREET:  Suite 500, 3000 K Street NW
;       CITY:  Washington
;       STATE:  DC
;       COUNTRY:  USA
;       ZIP:  20007
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/231,797
;       FILING DATE:
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/532,818
;       FILING DATE:  03-MAY-1996
;       APPLICATION NUMBER:  PCT/US94/04294
;       FILING DATE:  21-APR-1994
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  U.S. 08/143,364
;       FILING DATE:  29-OCT-1993
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  U.S. 08/051,741
;       FILING DATE:  23-APR-1993
;   ATTORNEY/AGENT INFORMATION:
;       NAME:  Isacson, John P.
;       REGISTRATION NUMBER:  33,751
;       REFERENCE/DOCKET NUMBER:  040433/0148
;   INFORMATION FOR SEQ ID NO:  93:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH:  10 amino acids
;           TYPE:  amino acid
;           TOPOLOGY:  linear
US-09-231-797-93

```

```

Query Match          41.9%;  Score 26;  DB 3;  Length 10;
Best Local Similarity 62.5%;  Pred. No. 1e+02;
Matches      5;  Conservative      0;  Mismatches      3;  Indels      0;  Gaps      0;

```

```

Qy      2 PQNFYKLP 9
        | |  |||
Db      2 PNNLDKLP 9

```

```

RESULT 22
US-08-934-224-93
; Sequence 93, Application US/08934224
; Patent No. 6100044
; GENERAL INFORMATION:

```

```

;   APPLICANT:  EVANS, Herbert J.
;   APPLICANT:  KINI, R. Manjunatha
;   TITLE OF INVENTION:  Polypeptides That Include Conformation-
;   TITLE OF INVENTION:  Constraining Groups Which Flank A Protein-Protein
Interaction
;   TITLE OF INVENTION:  Site
;   NUMBER OF SEQUENCES:  153
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Foley & Lardner
;       STREET:  Suite 500, 3000 K Street NW
;       CITY:  Washington
;       STATE:  DC
;       COUNTRY:  USA
;       ZIP:  20007
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/934,224
;       FILING DATE:
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/532,818
;       FILING DATE:  03-MAY-1996
;       APPLICATION NUMBER:  PCT/US94/04294
;       FILING DATE:  21-APR-1994
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  U.S. 08/143,364
;       FILING DATE:  29-OCT-1993
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  U.S. 08/051,741
;       FILING DATE:  23-APR-1993
;   ATTORNEY/AGENT INFORMATION:
;       NAME:  Isacson, John P.
;       REGISTRATION NUMBER:  33,751
;       REFERENCE/DOCKET NUMBER:  040433/0148
;   INFORMATION FOR SEQ ID NO:  93:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH:  10 amino acids
;           TYPE:  amino acid
;           TOPOLOGY:  linear
US-08-934-224-93

```

```

Query Match          41.9%;  Score 26;  DB 3;  Length 10;
Best Local Similarity 62.5%;  Pred. No. 1e+02;
Matches      5;  Conservative      0;  Mismatches      3;  Indels      0;  Gaps      0;

```

```

Qy          2 PQNFYKLP 9
             | |  |||
Db          2 PNNLDKLP 9

```

```

RESULT 23
US-08-933-843-93
; Sequence 93, Application US/08933843
; Patent No. 6111069

```

```

; GENERAL INFORMATION:
;   APPLICANT:  EVANS, Herbert J.
;   APPLICANT:  KINI, R. Manjunatha
;   TITLE OF INVENTION:  Polypeptides That Include Conformation-
;   TITLE OF INVENTION:  Constraining Groups Which Flank A Protein-Protein
Interaction
;   TITLE OF INVENTION:  Site
;   NUMBER OF SEQUENCES:  153
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Foley & Lardner
;     STREET:    Suite 500, 3000 K Street NW
;     CITY:      Washington
;     STATE:     DC
;     COUNTRY:   USA
;     ZIP:       20007
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:     IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:     PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/933,843
;     FILING DATE:        19-SEPT-1997
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/532,818
;     FILING DATE:        03-MAY-1996
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  U.S. 08/143,364
;     FILING DATE:        29-OCT-1993
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  U.S. 08/051,741
;     FILING DATE:        23-APR-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME:             Isacson, John P.
;     REGISTRATION NUMBER:  33,751
;     REFERENCE/DOCKET NUMBER:  040433/0148
;   INFORMATION FOR SEQ ID NO:  93:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:          10 amino acids
;       TYPE:             amino acid
;       TOPOLOGY:        linear
US-08-933-843-93

```

```

Query Match          41.9%;  Score 26;  DB 3;  Length 10;
Best Local Similarity 62.5%;  Pred. No. 1e+02;
Matches      5;  Conservative      0;  Mismatches      3;  Indels      0;  Gaps      0;

```

```

Qy      2 PQNFKLP 9
        | | |||
Db      2 PNNLDKLP 9

```

```

RESULT 24
US-08-934-223-93
; Sequence 93, Application US/08934223
; Patent No. 6147189
; GENERAL INFORMATION:

```

```

;   APPLICANT:  EVANS, Herbert J.
;   APPLICANT:  KINI, R. Manjunatha
;   TITLE OF INVENTION:  Polypeptides That Include Conformation-
;   TITLE OF INVENTION:  Constraining Groups Which Flank A Protein-Protein
Interaction
;   TITLE OF INVENTION:  Site
;   NUMBER OF SEQUENCES:  153
;   CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Foley & Lardner
;       STREET:  Suite 500, 3000 K Street NW
;       CITY:  Washington
;       STATE:  DC
;       COUNTRY:  USA
;       ZIP:  20007
;   COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/934,223
;       FILING DATE:
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/532,818
;       FILING DATE:  03-MAY-1996
;       APPLICATION NUMBER:  PCT/US94/04294
;       FILING DATE:  21-APR-1994
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  U.S. 08/143,364
;       FILING DATE:  29-OCT-1993
;   PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  U.S. 08/051,741
;       FILING DATE:  23-APR-1993
;   ATTORNEY/AGENT INFORMATION:
;       NAME:  Isacson, John P.
;       REGISTRATION NUMBER:  33,751
;       REFERENCE/DOCKET NUMBER:  040433/0148
;   INFORMATION FOR SEQ ID NO:  93:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH:  10 amino acids
;           TYPE:  amino acid
;           TOPOLOGY:  linear
US-08-934-223-93

```

```

Query Match          41.9%;  Score 26;  DB 3;  Length 10;
Best Local Similarity 62.5%;  Pred. No. 1e+02;
Matches      5;  Conservative    0;  Mismatches    3;  Indels      0;  Gaps      0;

```

```

Qy      2 PQNFYKLP 9
        | |  |||
Db      2 PNNLDKLP 9

```

```

RESULT 25
US-09-413-492-93
; Sequence 93, Application US/09413492
; Patent No. 6258550

```

```

; GENERAL INFORMATION:
;   APPLICANT:  EVANS, Herbert J.
;   APPLICANT:  KINI, R. Manjunatha
;   TITLE OF INVENTION:  Polypeptides That Include Conformation-
;   TITLE OF INVENTION:  Constraining Groups Which Flank A Protein-Protein
Interaction
;   TITLE OF INVENTION:  Site
;   NUMBER OF SEQUENCES:  153
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Foley & Lardner
;     STREET:  Suite 500, 3000 K Street NW
;     CITY:  Washington
;     STATE:  DC
;     COUNTRY:  USA
;     ZIP:  20007
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/413,492
;     FILING DATE:
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/532,818
;     FILING DATE:  03-MAY-1996
;     APPLICATION NUMBER:  PCT/US94/04294
;     FILING DATE:  21-APR-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  U.S. 08/143,364
;     FILING DATE:  29-OCT-1993
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  U.S. 08/051,741
;     FILING DATE:  23-APR-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Isacson, John P.
;     REGISTRATION NUMBER:  33,751
;     REFERENCE/DOCKET NUMBER:  040433/0148
;   INFORMATION FOR SEQ ID NO:  93:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  10 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
US-09-413-492-93

```

```

Query Match          41.9%;  Score 26;  DB 3;  Length 10;
Best Local Similarity 62.5%;  Pred. No. 1e+02;
Matches      5;  Conservative    0;  Mismatches    3;  Indels      0;  Gaps      0;

```

```

Qy      2 PQNFYKLP 9
        | | |||
Db      2 PNNLDKLP 9

```

```

RESULT 26
US-08-704-655-18
; Sequence 18, Application US/08704655

```



```

; Patent No. 5869453
; GENERAL INFORMATION:
;   APPLICANT: Moss, Denis J.
;   APPLICANT: Burrows, Scott R.
;   APPLICANT: Khanna, Rajiv
;   APPLICANT: Kerr, Veberly M.
;   APPLICANT: Burrows, Jacqueline M.
;   APPLICANT: Suhrbier, Andreas
;   TITLE OF INVENTION: Cytotoxic T Cell Epitopes
;   NUMBER OF SEQUENCES: 36
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: ARNOLD, WHITE & DURKEE
;     STREET: P.O. Box 4433
;     CITY: Houston
;     STATE: Texas
;     COUNTRY: USA
;     ZIP: 77210-4433
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/704,655
;     FILING DATE: 13-SEP-1996
;     CLASSIFICATION: 514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: PCT/AU95/00140
;     FILING DATE: 16-MAR-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Highlander, Steven L.
;     REGISTRATION NUMBER: 37,642
;     REFERENCE/DOCKET NUMBER: FBRC002
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (512) 418-3000
;     TELEFAX: (712) 789-2679
;   INFORMATION FOR SEQ ID NO: 18:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 11 amino acids
;       TYPE: amino acid
;       STRANDEDNESS:
;       TOPOLOGY: linear
US-08-704-655-18

```

```

Query Match          41.9%; Score 26; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
Matches      4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      5 FYKLPQM 11
        || :| |
Db      3 FYNIPPM 9

```

```

RESULT 27
US-08-462-436-22
; Sequence 22, Application US/08462436
; Patent No. 6001823

```

```

; GENERAL INFORMATION:
;   APPLICANT:  HULTGREN, Scott
;   TITLE OF INVENTION:  A NEW METHOD FOR THE TREATMENT AND
;   TITLE OF INVENTION:  PROPHYLAXIS OF BACTERIAL INFECTIONS
;   NUMBER OF SEQUENCES:  27
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  BROWDY AND NEIMARK
;     STREET:  419 Seventh Street, N.W., Suite 300
;     CITY:  Washington
;     STATE:  D.C.
;     COUNTRY:  USA
;     ZIP:  20004
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/462,436
;     FILING DATE:  05-JUN-1995
;     CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  PCT/US94/13455
;     FILING DATE:  18-NOV-1994
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  US 08/154,035
;     FILING DATE:  18-NOV-1993
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  COOPER, Iver P.
;     REGISTRATION NUMBER:  28,005
;     REFERENCE/DOCKET NUMBER:  HULTGREN=1C
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  202-628-5197
;     TELEFAX:  202-737-3528
;     TELEX:  248633
;   INFORMATION FOR SEQ ID NO:  22:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  16 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-462-436-22

```

```

Query Match          41.9%;  Score 26;  DB 3;  Length 16;
Best Local Similarity 57.1%;  Pred. No. 1.7e+02;
Matches      4;  Conservative    2;  Mismatches    1;  Indels      0;  Gaps      0;

```

```

Qy          3 QNFYKLP 9
             |: ||:|
Db          9 QDHYKMP 15

```

```

RESULT 28
US-08-465-275-22
; Sequence 22, Application US/08465275
; Patent No. 6153396

```

```

; GENERAL INFORMATION:
;   APPLICANT: HULTGREN, Scott
;   APPLICANT: KUEHN, Meta
;   APPLICANT: XU, Zheng
;   APPLICANT: OGG, Derek
;   APPLICANT: HARRIS, Mark
;   APPLICANT: LEPISTO, Matti
;   APPLICANT: KIHLEBERG, Jan
;   APPLICANT: JONES, Charles H.
;   TITLE OF INVENTION: TREATMENT OR PROPHYLAXIS OF DISEASES
;   TITLE OF INVENTION: CAUSED BY PILUS-FORMING BACTERIA
;   NUMBER OF SEQUENCES: 27
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
;     STREET: P.O. Box 1404
;     CITY: Alexandria
;     STATE: Virginia
;     COUNTRY: United States
;     ZIP: 22313-1404
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/465,275
;     FILING DATE: 05-JUN-1995
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US 08/154,035
;     FILING DATE: 18-NOV-1993
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: WO PCT/US94/13455
;     FILING DATE: 18-NOV-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Rea, Teresa Stanek
;     REGISTRATION NUMBER: 30,427
;     REFERENCE/DOCKET NUMBER: 016921-123
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (703) 836-6620
;     TELEFAX: (703) 836-2021
;   INFORMATION FOR SEQ ID NO: 22:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 16 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
US-08-465-275-22

```

```

Query Match          41.9%;  Score 26;  DB 3;  Length 16;
Best Local Similarity 57.1%;  Pred. No. 1.7e+02;
Matches      4;  Conservative    2;  Mismatches    1;  Indels      0;  Gaps      0;

```

```

Qy      3 QNFYKLP 9
        |:||:|
Db      9 QDHYKMP 15

```

RESULT 29

US-08-640-877-22

; Sequence 22, Application US/08640877

; Patent No. 6420127

; GENERAL INFORMATION:

; APPLICANT: HULTGREN, Scott

; APPLICANT: KUEHN, Meta

; APPLICANT: XU, Zheng

; APPLICANT: OGG, Derek

; APPLICANT: HARRIS, Mark

; APPLICANT: LEPISTO, Matti

; APPLICANT: KIHLEBERG, Jan

; APPLICANT: JONES, Charles H.

; TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS

; TITLE OF INVENTION: FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL

INFECTIONS

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/640,877

; FILING DATE: 10-OCT-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US94/13455

; FILING DATE: 18-NOV-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Rea, Teresa Stanek

; REGISTRATION NUMBER: 30,427

; REFERENCE/DOCKET NUMBER: 016921-122

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-640-877-22

Query Match 41.9%; Score 26; DB 4; Length 16;

Best Local Similarity 57.1%; Pred. No. 1.7e+02;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 QNFYKLP 9
|: ||:|
Db 9 QDHYKMP 15

RESULT 30

US-09-799-576A-22

; Sequence 22, Application US/09799576A

; Patent No. 6548265

; GENERAL INFORMATION:

; APPLICANT: HULTGREN, Scott

; KUEHN, Meta

; XU, Zheng

; OGG, Derek

; HARRIS, Mark

; LEPISTO, Matti

; KIHLEBERG, Jan

; JONES, Charles H.

; TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS

; FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL
INFECTIONS

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/799,576A

; FILING DATE: 07-Mar-2001

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/640,877

; FILING DATE: 10-OCT-1996

; APPLICATION NUMBER: WO PCT/US94/13455

; FILING DATE: 18-NOV-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Rea, Teresa Stanek

; REGISTRATION NUMBER: 30,427

; REFERENCE/DOCKET NUMBER: 016921-164

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-799-576A-22

Query Match 41.9%; Score 26; DB 4; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 QNFYKLP 9
|: ||:|
Db 9 QDHYKMP 15

RESULT 31

US-09-799-540-22

; Sequence 22, Application US/09799540

; Patent No. 6596504

; GENERAL INFORMATION:

; APPLICANT: HULTGREN, Scott

; APPLICANT: KUEHN, Meta

; APPLICANT: XU, Zheng

; APPLICANT: OGG, Derek

; APPLICANT: HARRIS, Mark

; APPLICANT: LEPISTO, Matti

; APPLICANT: KIHLEBERG, Jan

; APPLICANT: JONES, Charles H.

; TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS

; TITLE OF INVENTION: FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL
INFECTIONS

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/799,540

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/640,877

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Rea, Teresa Stanek

; REGISTRATION NUMBER: 30,427

; REFERENCE/DOCKET NUMBER: 016921-122

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-799-540-22

Query Match 41.9%; Score 26; DB 4; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 QNFYKLP 9
|: ||:|
Db 9 QDHYKMP 15

RESULT 32

US-08-765-061-9

; Sequence 9, Application US/08765061
; Patent No. 5935796
; GENERAL INFORMATION:
; APPLICANT: FOSANG, AMANDA J
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND COMPOSITIONS
; TITLE OF INVENTION: RELATING TO THE PROTEOGLYCAN PROTEINS OF CARTILAGE
; TITLE OF INVENTION: BREAKDOWN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRIFFITH HACK
; STREET: 509 ST KILDA ROAD
; CITY: MELBOURNE
; STATE: VICTORIA
; COUNTRY: AUSTRALIA
; ZIP: 3004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,061
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PM6668
; FILING DATE: 07-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SANTER, VIVIEN B
; REFERENCE/DOCKET NUMBER: FP4262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: +61 3 9243 8300
; TELEFAX: +61 3 9 243 8333/4
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant

; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: C-terminal
US-08-765-061-9

Query Match 40.3%; Score 25; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFY 6
:|:|:
Db 2 IPENFF 7

RESULT 33

US-09-514-739-2

; Sequence 2, Application US/09514739
; Patent No. 6379946
; GENERAL INFORMATION:
; APPLICANT: Ensign, Jerald C
; APPLICANT: Bowen, David J
; APPLICANT: Tenor, Jennifer L
; APPLICANT: Ciche, Todd A
; APPLICANT: Petell, James K.
; APPLICANT: Strickland, James A
; APPLICANT: Orr, Gregory L
; APPLICANT: Fatig, Raymond
; APPLICANT: Bintrim, Scott
; TITLE OF INVENTION: INSECTICIDAL PROTEIN TOXINS FROM XENORHABDUS
; FILE REFERENCE: 50585A
; CURRENT APPLICATION NUMBER: US/09/514,739
; CURRENT FILING DATE: 2000-02-28
; EARLIER APPLICATION NUMBER: 09/072,264
; EARLIER FILING DATE: 1998-05-04
; EARLIER APPLICATION NUMBER: 60/045,641
; EARLIER FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Xenorhabdus Wi
US-09-514-739-2

Query Match 40.3%; Score 25; DB 4; Length 8;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 QNFYKLP 9
|||:
Db 2 QNVYRYP 8

RESULT 34

US-07-954-213-4

; Sequence 4, Application US/07954213


```

; Patent No. 5387504
; GENERAL INFORMATION:
;   APPLICANT: Mumford, Richard A.
;   APPLICANT: Lark, Michael W.
;   APPLICANT: Bayne, Ellen B.K.
;   APPLICANT: Hoerrner, Lori A.
;   TITLE OF INVENTION: MONOSPECIFIC ANTIBODIES AND ASSAY SYSTEM
;   TITLE OF INVENTION: FOR DETECTING STROMELYSIN CLEAVAGE PRODUCTS
;   NUMBER OF SEQUENCES: 24
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Merck & Co., Inc.
;     STREET: 126 E. Lincoln Avenue
;     CITY: Rahway
;     STATE: NJ
;     COUNTRY: USA
;     ZIP: 07065
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/07/954,213
;     FILING DATE: 19920930
;     CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Wallen, John W.III
;     REGISTRATION NUMBER: 35,403
;     REFERENCE/DOCKET NUMBER: 18842
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (908) 594-3905
;     TELEFAX: (908) 594-4720
;   INFORMATION FOR SEQ ID NO: 4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 10 amino acids
;       TYPE: AMINO ACID
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
US-07-954-213-4

```

```

Query Match          40.3%; Score 25; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches      3; Conservative      3; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 MPQNFY 6
        :|:|:
Db      2 IPENFF 7

```

```

RESULT 35
US-08-765-061-7
; Sequence 7, Application US/08765061
; Patent No. 5935796
; GENERAL INFORMATION:
;   APPLICANT: FOSANG, AMANDA J
;   TITLE OF INVENTION: DIAGNOSTIC METHODS AND COMPOSITIONS

```

```

; TITLE OF INVENTION: RELATING TO THE PROTEOGLYCAN PROTEINS OF CARTILAGE
; TITLE OF INVENTION: BREAKDOWN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRIFFITH HACK
; STREET: 509 ST KILDA ROAD
; CITY: MELBOURNE
; STATE: VICTORIA
; COUNTRY: AUSTRALIA
; ZIP: 3004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,061
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PM6668
; FILING DATE: 07-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SANTER, VIVIEN B
; REFERENCE/DOCKET NUMBER: FP4262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: +61 3 9243 8300
; TELEFAX: +61 3 9 243 8333/4
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: C-terminal
US-08-765-061-7

```

```

Query Match          40.3%; Score 25; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches      3; Conservative      3; Mismatches      0; Indels      0; Gaps      0;

```

```

Qy      1 MPQNFY 6
        :|:|:
Db      2 IPENFF 7

```

```

RESULT 36
US-07-737-371E-39
; Sequence 39, Application US/07737371E
; Patent No. 5876948
; GENERAL INFORMATION:
; APPLICANT: Yankner, Bruce A.
; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)

```

```

; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-737-371E-39

```

```

Query Match          40.3%; Score 25; DB 2; Length 11;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches      5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      2 PQNFYKL 8
        || || |
Db      4 PQCFYAL 10

```

RESULT 37

US-07-737-371E-40

; Sequence 40, Application US/07737371E

; Patent No. 5876948

; GENERAL INFORMATION:

; APPLICANT: Yankner, Bruce A.

; TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY

; TITLE OF INVENTION: NEUROTOXIN INHIBITORS (AS AMENDED)

; NUMBER OF SEQUENCES: 77

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson, P.C.

; STREET: 225 Franklin Street

```

; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/737,371E
; FILING DATE: 29-JUL-1991
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/559,172
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00108/028002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-737-371E-40

```

```

Query Match          40.3%; Score 25; DB 2; Length 11;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches      5; Conservative      0; Mismatches      2; Indels      0; Gaps      0;

```

```

Qy      2 PQNFYKL 8
        || || |
Db      4 PQCFYPL 10

```

RESULT 38

US-09-579-883A-12

```

; Sequence 12, Application US/09579883A
; Patent No. 6686443
; GENERAL INFORMATION:
; APPLICANT: RABENSTEIN, DALLAS
; APPLICANT: SHI, TIESHENG
; TITLE OF INVENTION: CHEMICAL REAGENTS FOR FORMATION OF DISULFIDE BONDS IN
PEPTIDES
; FILE REFERENCE: 407T-891100US
; CURRENT APPLICATION NUMBER: US/09/579,883A
; CURRENT FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 11

```

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-579-883A-12

Query Match 40.3%; Score 25; DB 4; Length 11;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
|| || |
Db 4 PQCFYPL 10

RESULT 39

US-08-275-983B-17

; Sequence 17, Application US/08275983B
; Patent No. 5688665
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; APPLICANT: Roberts, James M.
; APPLICANT: Koff, Andrew
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: Isolated p27 Protein, Nucleic Acid Molecules
Encoding Sa

; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/275,983B
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/179,045
; FILING DATE: 07-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MII-079CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-275-983B-17

Query Match 40.3%; Score 25; DB 1; Length 12;
Best Local Similarity 30.0%; Pred. No. 1.9e+02;
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MPQNFYKLPQ 10
:|: :|: |:|:
Db 1 LPEFYRPPR 10

RESULT 40

US-08-794-002-10

; Sequence 10, Application US/08794002

; Patent No. 6316208

; GENERAL INFORMATION:

; APPLICANT: Roberts, James M.

; APPLICANT: Porter, Peggy L.

; TITLE OF INVENTION: ISOLATED P27 PROTEIN AND METHODS FOR ITS

; TITLE OF INVENTION: PRODUCTION AND USE

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HOAG & ELIOT LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109-2170

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/794,002

; FILING DATE: 03-FEB-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: MIV-079.03

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-832-1000

; TELEFAX: 617-832-7000

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 12 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-794-002-10

Query Match 40.3%; Score 25; DB 4; Length 12;

Best Local Similarity 30.0%; Pred. No. 1.9e+02;
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MPQNFYKLPQ 10
:|: :|: |:
Db 1 LPEFYRPPR 10

RESULT 41

US-08-854-039B-10

; Sequence 10, Application US/08854039B

; Patent No. 6355774

; GENERAL INFORMATION:

; APPLICANT: Massague, Joan

; APPLICANT: Roberts, James M.

; APPLICANT: Koff, Andrew

; APPLICANT: Polyak, Kornelia

; TITLE OF INVENTION: ISOLATED p27 PROTEIN AND METHOD FOR ITS

; TITLE OF INVENTION: PRODUCTION AND USE

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HOAG & ELIOT LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109-2170

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/854,039B

; FILING DATE: 09-MAY-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: MIV-079.04

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-832-1000

; TELEFAX: 617-832-7000

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 12 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-854-039B-10

Query Match 40.3%; Score 25; DB 4; Length 12;

Best Local Similarity 30.0%; Pred. No. 1.9e+02;

Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MPQNFYKLPQ 10
:|: :|: |:

Db 1 LPEFYRPPR 10

RESULT 42

US-08-765-702B-10

; Sequence 10, Application US/08765702B

; Patent No. 6635450

; GENERAL INFORMATION:

; APPLICANT: Massague, Joan

; Roberts, James M.

; Koff, Andrew

; Polyak, Kornelia

; TITLE OF INVENTION: ISOLATED p27 PROTEIN, NUCLEIC ACID

; MOLECULES ENCODING SAME, METHODS OF IDENTIFYING

AGENTS

; ACTING ON SAME, AND USES OF SAID AGENTS

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HOAG & ELIOT LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109-2170

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WordPad

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/765,702B

; FILING DATE: 28-Apr-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Vincent, Matthew P.

; REGISTRATION NUMBER: 36,709

; REFERENCE/DOCKET NUMBER: MIV-079.04

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-832-1000

; TELEFAX: 617-832-7000

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 12 amino acids

; TYPE: amino acid

; STRANDEDNESS: <Unknown>

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-08-765-702B-10

Query Match 40.3%; Score 25; DB 4; Length 12;

Best Local Similarity 30.0%; Pred. No. 1.9e+02;

Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MPQNFYKLPQ 10

:|: :|: |:

Db 1 LPEFYRPPR 10

RESULT 43

US-08-637-418-9

```
; Sequence 9, Application US/08637418
; Patent No. 5891848
; GENERAL INFORMATION:
;   APPLICANT: OOMURA, Yutaka
;   TITLE OF INVENTION: PEPTIDE FRAGMENTS
;   NUMBER OF SEQUENCES: 20
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Fisher, Christen & Sabol
;     STREET: 1019 19th St., N.W., Suite 300
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: U.S.A.
;     ZIP: 20036
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/637,418
;     FILING DATE: 25-APR-1996
;     CLASSIFICATION: 514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: JP 125,947/1995
;     FILING DATE: 25-APR-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Hollander, Barry I.
;     REGISTRATION NUMBER: 28,566
;     REFERENCE/DOCKET NUMBER: NZK-116
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (202) 659-2000
;     TELEFAX: (202) 659-2015
;   INFORMATION FOR SEQ ID NO: 9:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 15 amino acids
;       TYPE: amino acid
;       STRANDEDNESS:
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO
;     FRAGMENT TYPE: N-terminal
;     ORIGINAL SOURCE:
;       ORGANISM: Homo sapiens
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US-08-637-418-9

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Query Match          40.3%; Score 25; DB 2; Length 15;
Best Local Similarity 36.4%; Pred. No. 2.4e+02;
Matches      4; Conservative      3; Mismatches      4; Indels      0; Gaps      0;
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Qy      1 MPQNFYKLPQM 11
        :|  || |::
Db      3 LPPGNYKKPKL 13
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RESULT 44

US-08-637-418-10

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; Sequence 10, Application US/08637418
; Patent No. 5891848
; GENERAL INFORMATION:
;   APPLICANT: OOMURA, Yutaka
;   TITLE OF INVENTION: PEPTIDE FRAGMENTS
;   NUMBER OF SEQUENCES: 20
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Fisher, Christen & Sabol
;     STREET: 1019 19th St., N.W., Suite 300
;     CITY: Washington
;     STATE: D.C.
;     COUNTRY: U.S.A.
;     ZIP: 20036
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/637,418
;     FILING DATE: 25-APR-1996
;     CLASSIFICATION: 514
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: JP 125,947/1995
;     FILING DATE: 25-APR-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Hollander, Barry I.
;     REGISTRATION NUMBER: 28,566
;     REFERENCE/DOCKET NUMBER: NZK-116
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (202) 659-2000
;     TELEFAX: (202) 659-2015
;   INFORMATION FOR SEQ ID NO: 10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 15 amino acids
;       TYPE: amino acid
;       STRANDEDNESS:
;       TOPOLOGY: linear
;     MOLECULE TYPE: peptide
;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO
;     FRAGMENT TYPE: N-terminal
;     ORIGINAL SOURCE:
;       ORGANISM: Homo sapiens
;     FEATURE:
;       NAME/KEY: Modified-site
;       LOCATION: 15
;       OTHER INFORMATION: /product= "Xaa is the amide form of
;       OTHER INFORMATION: Tyrosine."
US-08-637-418-10
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Query Match          40.3%; Score 25; DB 2; Length 15;
Best Local Similarity 36.4%; Pred. No. 2.4e+02;
Matches      4; Conservative      3; Mismatches      4; Indels      0; Gaps      0;
```

Qy 1 MPQNFYKLPQM 11
:| |||::
Db 3 LPPGNYKKPKL 13

RESULT 45

US-07-954-213-12

; Sequence 12, Application US/07954213

; Patent No. 5387504

; GENERAL INFORMATION:

; APPLICANT: Mumford, Richard A.

; APPLICANT: Lark, Michael W.

; APPLICANT: Bayne, Ellen B.K.

; APPLICANT: Hoerrner, Lori A.

; TITLE OF INVENTION: MONOSPECIFIC ANTIBODIES AND ASSAY SYSTEM

; TITLE OF INVENTION: FOR DETECTING STROMELYSIN CLEAVAGE PRODUCTS

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Merck & Co., Inc.

; STREET: 126 E. Lincoln Avenue

; CITY: Rahway

; STATE: NJ

; COUNTRY: USA

; ZIP: 07065

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/954,213

; FILING DATE: 19920930

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Wallen, John W.III

; REGISTRATION NUMBER: 35,403

; REFERENCE/DOCKET NUMBER: 18842

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (908) 594-3905

; TELEFAX: (908) 594-4720

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; TYPE: AMINO ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-07-954-213-12

Query Match 40.3%; Score 25; DB 1; Length 16;

Best Local Similarity 50.0%; Pred. No. 2.6e+02;

Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFY 6

:|:|:

Db 9 IPENFF 14

RESULT 46

US-07-861-458C-134

; Sequence 134, Application US/07861458C

; Patent No. 6232061

; GENERAL INFORMATION:

; APPLICANT: Marchionni, Mark Andrew

; APPLICANT: Johnson, Carl D.

; TITLE OF INVENTION: HOMOLOGY CLONING

; NUMBER OF SEQUENCES: 142

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: U.S.A.

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM PS/2 Model 50Z or 55SX

; OPERATING SYSTEM: MS-DOS (Version 5.0)

; SOFTWARE: WordPerfect (Version 5.1)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/861,458C

; FILING DATE: 04/01/92

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Clark, Paul T.

; REGISTRATION NUMBER: 30,162

; REFERENCE/DOCKET NUMBER: 04585/014001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 542-5070

; TELEFAX: (617) 542-8906

; TELEX: 200154

; INFORMATION FOR SEQ ID NO: 134:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16

; TYPE: amino acid

; TOPOLOGY: linear

US-07-861-458C-134

Query Match 40.3%; Score 25; DB 3; Length 16;

Best Local Similarity 40.0%; Pred. No. 2.6e+02;

Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PQNFYKLPQM 11

| : | | : | :

Db 6 PKTFEKMAQL 15

RESULT 47

US-08-968-676-69

; Sequence 69, Application US/08968676

; Patent No. 5919639
; GENERAL INFORMATION:
; APPLICANT: Humphreys, Robert E
; APPLICANT: Adams, Sharlene
; APPLICANT: Xu, Minzhen
; TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
; NUMBER OF SEQUENCES: 165
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kevin M. Farrell, P.C.
; STREET: P.O. Box 999
; CITY: York Harbor
; STATE: ME
; COUNTRY: USA
; ZIP: 03911
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,676
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Farrell, Kevin M
; REGISTRATION NUMBER: 35,505
; REFERENCE/DOCKET NUMBER: REH-9601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (207) 363-0558
; TELEFAX: (207) 363-0528
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-968-676-69

Query Match 38.7%; Score 24; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YKLPQ 10
||||:
Db 3 YKLPK 7

RESULT 48 \

US-09-266-764-26
; Sequence 26, Application US/09266764
; Patent No. 6545139
; GENERAL INFORMATION:
; APPLICANT: Baylor College of Medicine
; TITLE OF INVENTION: Compositions and Methods For the Treatment and
; TITLE OF INVENTION: Prevention of Metastatic Disorders
; FILE REFERENCE: 00A146.0122

; CURRENT APPLICATION NUMBER: US/09/266,764
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/077,934
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-266-764-26

Query Match 38.7%; Score 24; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YKLPQ 10
|:| | |
Db 4 YQLPQ 8

RESULT 49

US-08-024-253-18

; Sequence 18, Application US/08024253

; Patent No. 5785968

; GENERAL INFORMATION:

; APPLICANT: KIMACHI, Kazuhiko

; APPLICANT: MAEDA, Hiroaki

; APPLICANT: NISHIYAMA, Kiyoto

; APPLICANT: TOKIYOSHI, Sachio

; APPLICANT: TOHYA, Yukinobu

; APPLICANT: MIKAMI, Takeshi

; TITLE OF INVENTION: ANTI-FELINE CALCIVIRUS RECOMBINANT

; TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT ENCODING THE SAME

; NUMBER OF SEQUENCES: 23

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: WEGNER, CANTOR, MUELLER & PLAYER

; STREET: 1233 20th Street, N.W., Suite 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20036-8218

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/024,253

; FILING DATE: 19930301

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 79189/1992

; FILING DATE: 28-FEB-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: CANTOR, Herbert I.

; REGISTRATION NUMBER: 24,392

; REFERENCE/DOCKET NUMBER: P-500-23744
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-0400
; TELEFAX: (202) 835-0605
; TELEX: 440706 WEGBR
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-024-253-18

Query Match 38.7%; Score 24; DB 1; Length 9;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 QNFYKLP 9
|||: |
Db 1 QNFWTTP 7

RESULT 50

US-08-629-291A-27

; Sequence 27, Application US/08629291A
; Patent No. 5959174

; GENERAL INFORMATION:

; APPLICANT: Coruzzi, Gloria
; APPLICANT: Oliveira, Igor
; APPLICANT: Lam, Hon-Ming
; APPLICANT: Hsieh, Ming-Hsuin
; TITLE OF INVENTION: PLANT GLUTAMATE RECEPTORS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/629,291A
; FILING DATE: 08-APR-1996
; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 5914-050

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-629-291A-27

Query Match 38.7%; Score 24; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QNFYK 7
|:|
Db 5 QSFYK 9

Search completed: July 4, 2004, 04:48:49
Job time : 7.89552 secs

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:35:16 ; Search time 8.45522 Seconds
(without alignments)
125.142 Million cell updates/sec

Title: US-09-641-802-6
Perfect score: 62
Sequence: 1 MPQNFYKLPQM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2898

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

8							
Result	Query						
No.	Score	Match	Length	DB	ID	Description	
1	25	40.3	17	2	S57991	hydroxyproline-ric	
2	24	38.7	12	2	PH1454	T-cell receptor al	
3	24	38.7	13	2	PH0787	T-cell receptor al	
4	23	37.1	11	1	SPHO	substance P - hors	
5	23	37.1	11	1	A60654	substance P - guin	
6	23	37.1	11	2	JN0023	substance P - chic	
7	22	35.5	11	2	S07201	physalaemin - frog	
8	22	35.5	11	2	A61033	ranatachykinin A -	
9	22	35.5	11	2	D61033	ranatachykinin D -	
10	22	35.5	15	2	A48372	benzoyl-CoA ligase	
11	21	33.9	8	2	A39892	P element, P cytot	
12	21	33.9	9	2	PT0270	Ig heavy chain CRD	
13	21	33.9	12	2	B60228	Fc mu (IgM) recept	

14	20	32.3	7	2	B44787	calliFMRFamide 11
15	20	32.3	11	2	S07203	uperolein - frog (
16	20	32.3	11	4	I52708	ELAV-like neuronal
17	20	32.3	12	2	S07436	tachykinin - Afric
18	20	32.3	12	2	A09985	gamma-crystallin -
19	20	32.3	12	2	S57570	T cell receptor V-
20	20	32.3	12	2	S74144	aggrecan - bovine
21	20	32.3	16	2	T37075	hypothetical prote
22	19	30.6	10	2	C39398	Fc mu (IgM) recept
23	19	30.6	11	2	S23306	substance P - Atla
24	19	30.6	11	2	S23373	T-cell receptor al
25	19	30.6	13	2	S47358	T-cell antigen rec
26	19	30.6	15	2	PA0008	lectin B2 - Psopho
27	19	30.6	15	2	A36279	chemoattractant pr
28	19	30.6	15	2	S51735	T-cell receptor be
29	19	30.6	15	2	B49655	T-cell-receptor be
30	19	30.6	16	2	S22040	cob protein - comm
31	19	30.6	16	2	PH1778	T cell receptor al
32	19	30.6	16	2	E49255	T-cell receptor be
33	19	30.6	16	2	F49039	T-cell receptor be
34	19	30.6	18	2	S23971	alpha-macroglobuli
35	18	29.0	8	2	B24749	neuropeptide B - b
36	18	29.0	8	2	I49404	prealbumin - weste
37	18	29.0	11	2	F60409	substance P-like p
38	18	29.0	11	2	E60409	substance P-like p
39	18	29.0	11	2	S23308	substance P - rain
40	18	29.0	13	2	S01119	photosystem II pro
41	18	29.0	13	4	I70076	glycophorin B/glyc
42	18	29.0	14	2	B36079	hypothetical prote
43	18	29.0	14	2	S58862	botulinum neurotox
44	18	29.0	14	2	S58866	botulinum neurotox
45	18	29.0	14	2	PL0152	metal-binding prot
46	18	29.0	14	2	B20872	alpha-2-macroglobu
47	18	29.0	14	2	PT0294	Ig heavy chain CRD
48	18	29.0	15	2	S08209	hypothetical prote
49	18	29.0	15	2	A56049	urinary tract ston
50	18	29.0	15	4	I38335	hypothetical TEL/M
51	18	29.0	16	2	S65520	phospholipase A2 (
52	18	29.0	18	2	PN0149	beta-Gliadine 13 -
53	18	29.0	18	2	A24749	neuropeptide A - b
54	17.5	28.2	11	2	PC2330	cycloinulooligosac
55	17	27.4	9	2	D58503	translation elonga
56	17	27.4	11	2	S53436	beta-D-galactosida
57	17	27.4	13	2	S29488	GTP-binding protei
58	17	27.4	14	2	H64008	hypothetical prote
59	17	27.4	14	2	PA0101	protein QF200020 -
60	17	27.4	14	2	S29486	GTP-binding protei
61	17	27.4	15	2	PA0088	protein QF200051 -
62	17	27.4	15	2	C36198	T-cell receptor be
63	17	27.4	15	2	PQ0073	T-cell receptor be
64	17	27.4	16	2	A24099	crystal protein, 2
65	17	27.4	16	2	C39509	mannose-specific l
66	17	27.4	16	2	I46275	hemoglobin beta-x
67	17	27.4	17	2	I78870	gene RB1 protein -
68	17	27.4	18	2	I51427	hemoglobin alpha c
69	17	27.4	18	2	S29264	ovohemerythrin - d
70	17	27.4	18	2	A60915	enkephalin-degradi

71	17	27.4	18	2	A30541	F7-1 fimbrial prot
72	17	27.4	18	2	B44995	alkanal monooxygen
73	17	27.4	18	2	S09722	2S albumin small c
74	16	25.8	8	2	S16324	hypothetical prote
75	16	25.8	9	2	C36730	hutU protein - Kle
76	16	25.8	9	2	PT0080	60K Ca binding pro
77	16	25.8	9	2	PT0285	Ig heavy chain CRD
78	16	25.8	10	2	B61033	ranatachykinin B -
79	16	25.8	11	2	S68392	H+-transporting tw
80	16	25.8	11	2	A38590	transforming prote
81	16	25.8	11	2	F33098	214K exoantigen (v
82	16	25.8	11	2	S33300	probable substance
83	16	25.8	12	2	E45691	probable minor cap
84	16	25.8	12	2	PA0047	protein QA100045 -
85	16	25.8	13	2	S21152	tryptophyllin-rela
86	16	25.8	13	2	A59387	VCAM-1 5'UTR bindi
87	16	25.8	14	2	C60414	somatostatin - sli
88	16	25.8	14	2	B60842	somatostatin I - c
89	16	25.8	14	2	A60840	somatostatin I - E
90	16	25.8	14	2	S00172	somatostatin I - s
91	16	25.8	14	2	PL0142	carbon-monoxide de
92	16	25.8	14	2	PT0254	Ig heavy chain CRD
93	16	25.8	14	2	JS0272	hypothetical 1.5K
94	16	25.8	14	2	PC4382	dehydrin 4.5K poly
95	16	25.8	15	2	I52734	gene c-Ki-ras prot
96	16	25.8	15	2	PA0005	lectin A1 - Psopho
97	16	25.8	15	2	PH1762	T cell receptor al
98	16	25.8	15	2	D46743	corneal keratan su
99	16	25.8	15	2	I65478	c-Ki-ras - hamster
100	16	25.8	15	2	PH0784	T-cell receptor al

ALIGNMENTS

RESULT 1

S57991

hydroxyproline-rich protein - *Sesbania rostrata* (fragment)

C;Species: *Sesbania rostrata*

C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 11-Jan-2000

C;Accession: S57991

R;Goormachtig, S.; Valerio-Lepiniec, M.; Szczygłowski, K.; van Montagu, M.; Holsters, M.; de Bruijn, F.

submitted to the EMBL Data Library, March 1995

A;Description: Use of differential display to identify novel *Sesbania rostrata* genes enhanced by *Azorhizobium caulinodans* infection.

A;Reference number: S57991

A;Accession: S57991

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-17 <GOO>

A;Cross-references: EMBL:Z48673; NID:g899484; PID:g899485

C;Superfamily: hydroxyproline-rich glycoprotein

Query Match 40.3%; Score 25; DB 2; Length 17;

Best Local Similarity 50.0%; Pred. No. 2e+02;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PQNFYKLP 9
| :|||
Db 3 PHYYYKSP 10

RESULT 2

PH1454

T-cell receptor alpha chain (clone A3/72.2) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995

C;Accession: PH1454

R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.;

Regnault, A.; Kourilsky, P.; Cerottini, J.C.; Maryanski, J.L.

J. Exp. Med. 177, 811-820, 1993

A;Title: T cell receptor selection by and recognition of two class I major histocompatibility complex-restricted antigenic peptides that differ at a single position.

A;Reference number: PH1430; MUID:93171821; PMID:8436911

A;Accession: PH1454

A;Molecule type: mRNA

A;Residues: 1-12 <CAS>

A;Experimental source: cytolytic T-lymphocyte

C;Superfamily: immunoglobulin homology

C;Keywords: receptor; T-cell

Query Match 38.7%; Score 24; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QNFY 6
||||
Db 7 QNFY 10

RESULT 3

PH0787

T-cell receptor alpha chain (F8) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PH0787

R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A;Title: T cell receptor genes in a series of class I major histocompatibility complex-restricted cytotoxic T lymphocyte clones specific for a Plasmodium berghei nonapeptide: implications for T cell allelic exclusion and antigen-specific repertoire.

A;Reference number: PH0746; MUID:92078846; PMID:1836010

A;Accession: PH0787

A;Molecule type: mRNA

A;Residues: 1-13 <CAS>

A;Cross-references: EMBL:X60891

A;Experimental source: T lymphocyte

C;Keywords: T-cell receptor

Query Match 38.7%; Score 24; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QNFY 6
||||
Db 8 QNFY 11

RESULT 4

SPHO

substance P - horse

C;Species: Equus caballus (domestic horse)

C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 23-Aug-1996

C;Accession: A01558

R;Studer, R.O.; Trzeciak, A.; Lergier, W.

Helv. Chim. Acta 56, 860-866, 1973

A;Title: Isolierung und Aminosaeuresequenz von Substanz P aus Pferdedarm.

A;Reference number: A01558

A;Accession: A01558

A;Molecule type: protein

A;Residues: 1-11 <STU>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; hormone

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 37.1%; Score 23; DB 1; Length 11;

Best Local Similarity 57.1%; Pred. No. 3.1e+02;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
|| |: |
Db 4 PQQFFGL 10

RESULT 5

A60654

substance P - guinea pig

C;Species: Cavia porcellus (guinea pig)

C;Date: 14-May-1993 #sequence_revision 27-Jun-1994 #text_change 08-Dec-1995

C;Accession: A60654

R;Murphy, R.

Neuropeptides 14, 105-110, 1989

A;Title: Primary amino acid sequence of guinea-pig substance P.

A;Reference number: A60654; MUID:90044685; PMID:2478925

A;Accession: A60654

A;Molecule type: protein

A;Residues: 1-11 <MUR>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 37.1%; Score 23; DB 1; Length 11;

Best Local Similarity 57.1%; Pred. No. 3.1e+02;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
|| |: |
Db 4 PQQFFGL 10

RESULT 6

JN0023

substance P - chicken

C;Species: Gallus gallus (chicken)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jul-1997

C;Accession: JN0023

R;Conlon, J.M.; Katsoulis, S.; Schmidt, W.E.; Thim, L.

Regul. Pept. 20, 171-180, 1988

A;Title: [Arg3]substance P and neurokinin A from chicken small intestine.

A;Reference number: JN0023; MUID:88204263; PMID:2452461

A;Accession: JN0023

A;Molecule type: protein

A;Residues: 1-11 <CON>

C;Superfamily: substance P precursor

C;Keywords: amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 37.1%; Score 23; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
|||:|
Db 4 PQQFFGL 10

RESULT 7

S07201

physalaemin - frog (Physalaemus fuscumaculatus)

C;Species: Physalaemus fuscumaculatus

C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000

C;Accession: S07201

R;Erspamer, V.; Anastasi, A.; Bertaccini, G.; Cei, J.M.

Experientia 20, 489-490, 1964

A;Title: Structure and pharmacological actions of physalaemin, the main active polypeptide of the skin of Physalaemus fuscumaculatus.

A;Reference number: S07201; MUID:66076612; PMID:5857249

A;Accession: S07201

A;Molecule type: protein

A;Residues: 1-11 <ERS>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 35.5%; Score 22; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
| |||
Db 4 PNKFYGL 10

RESULT 8

A61033
 ranatachykinin A - bullfrog
 C;Species: Rana catesbeiana (bullfrog)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
 C;Accession: A61033; JE0426
 R;Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.
 Regul. Pept. 42(Suppl.1), S12, 1992
 A;Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.
 A;Reference number: A61033
 A;Accession: A61033
 A;Molecule type: protein
 A;Residues: 1-11 <KAN>
 R;Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.
 Biochem. Biophys. Res. Commun. 177, 588-595, 1991
 A;Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.
 A;Reference number: JE0426; MUID:91254337; PMID:2043143
 A;Accession: JE0426
 A;Molecule type: protein
 A;Residues: 1-11 <KOZ>
 C;Superfamily: unassigned animal peptides
 C;Keywords: amidated carboxyl end; neuropeptide
 F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 35.5%; Score 22; DB 2; Length 11;
 Best Local Similarity 57.1%; Pred. No. 4.8e+02;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
 | |||
 Db 4 PDRFYGL 10

RESULT 9
 D61033
 ranatachykinin D - bullfrog
 C;Species: Rana catesbeiana (bullfrog)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 18-Aug-2000
 C;Accession: D61033; JE0429
 R;Kangawa, K.; Kozawa, H.; Hino, J.; Minamino, N.; Matsuo, H.
 Regul. Pept. 42(Suppl.1), S12, 1992
 A;Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.
 A;Reference number: A61033
 A;Accession: D61033
 A;Molecule type: protein
 A;Residues: 1-11 <KAN>
 R;Kozawa, H.; Hino, J.; Minamino, N.; Kangawa, K.; Matsuo, H.
 Biochem. Biophys. Res. Commun. 177, 588-595, 1991
 A;Title: Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.
 A;Reference number: JE0426; MUID:91254337; PMID:2043143
 A;Accession: JE0429
 A;Molecule type: protein
 A;Residues: 1-11 <KOZ>
 C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; neuropeptide
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 35.5%; Score 22; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 4.8e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PQNFY 6
|: ||
Db 4 PERFY 8

RESULT 10

A48372

benzoyl-CoA ligase - Methanospirillum hungatei (fragment)

C;Species: Methanospirillum hungatei

C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-May-1999

C;Accession: A48372

R;Auburger, G.; Winter, J.

Appl. Microbiol. Biotechnol. 37, 789-795, 1992

A;Title: Purification and characterization of benzoyl-CoA ligase from a
syntrophic, benzoate-degrading, anaerobic mixed culture.

A;Reference number: A48372; MUID:93040109; PMID:1369492

A;Accession: A48372

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <AUB>

A;Note: sequence extracted from NCBI backbone (NCBIP:118357)

Query Match 35.5%; Score 22; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 6.6e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PQNFY 6
|: ||
Db 5 PEEFY 9

RESULT 11

A39892

P element, P cytotype-determining - fruit fly (Drosophila melanogaster)
(fragment)

C;Species: Drosophila melanogaster

C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Feb-1997

C;Accession: A39892

R;Nitasaka, E.; Mukai, T.; Yamazaki, T.

Proc. Natl. Acad. Sci. U.S.A. 84, 7605-7608, 1987

A;Title: Repressor of P elements in Drosophila melanogaster: cytotype
determination by a defective P element carrying only open reading frames 0
through 2.

A;Reference number: A39892

A;Accession: A39892

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-8 <NIT>

C;Genetics:

A;Gene: FlyBase:P-element

A;Cross-references: FlyBase:FBgn0003055

Query Match 33.9%; Score 21; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNF 5
:|:|
Db 1 IPKNF 5

RESULT 12

PT0270

Ig heavy chain CRD3 region (clone 3-100) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0270

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain
diversity and joining segments in adult human peripheral blood B lymphocytes.

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0270

A;Molecule type: DNA

A;Residues: 1-9 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 33.9%; Score 21; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QNFY 6
||:|
Db 1 QNYY 4

RESULT 13

B60228

Fc mu (IgM) receptor surface complex beta chain - mouse (fragment)

N;Alternate names: membrane protein B29

C;Species: Mus musculus (house mouse)

C;Date: 08-Dec-1992 #sequence_revision 08-Dec-1992 #text_change 20-Mar-1998

C;Accession: B60228; B39398

R;Hombach, J.; Lottspeich, F.; Reth, M.
Eur. J. Immunol. 20, 2795-2799, 1990

A;Title: Identification of the genes encoding the IgM-alpha and Ig-beta
components of the IgM antigen receptor complex by amino-terminal sequencing.

A;Reference number: A60228; MUID:91099432; PMID:2269334

A;Accession: B60228

A;Molecule type: protein

A;Residues: 1-12 <HOM>

R;Campbell, K.S.; Hager, E.J.; Friedrich, R.J.; Cambier, J.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 3982-3986, 1991

A;Title: IgM antigen receptor complex contains phosphoprotein products of B29
and mb-1 genes.

A;Reference number: A39398; MUID:91219496; PMID:2023945

A;Accession: B39398
A;Molecule type: protein
A;Residues: 'XX',3-10 <CAM>
C;Keywords: membrane protein

Query Match 33.9%; Score 21; DB 2; Length 12;
Best Local Similarity 44.4%; Pred. No. 8.1e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPQNFYKLP 9
:| || |
Db 4 LPLNFQGSP 12

RESULT 14

B44787

calliFMRFamide 11 - bluebottle fly (*Calliphora vomitoria*)

C;Species: *Calliphora vomitoria*

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999

C;Accession: B44787

R;Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe, A.

Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992

A;Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (designated calliFMRFamides) from the blowfly *Calliphora vomitoria*.

A;Reference number: A41978; MUID:92196111; PMID:1549595

A;Accession: B44787

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-7 <DUV>

C;Keywords: amidated carboxyl end; neuropeptide

F;7/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 32.3%; Score 20; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYK 7
| || :
Db 1 PDNEMR 6

RESULT 15

S07203

uperolein - frog (*Uperoleia marmorata*)

C;Species: *Uperoleia marmorata*

C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 18-Aug-2000

C;Accession: S07203

R;Anastasi, A.; Erspamer, V.; Endean, R.

Experientia 31, 394-395, 1975

A;Title: Structure of uperolein, a physalaemin-like endecapeptide occurring in the skin of *Uperoleia rugosa* and *Uperoleia marmorata*.

A;Reference number: S07203; MUID:75131227; PMID:1120493

A;Accession: S07203

A;Molecule type: protein

A;Residues: 1-11 <ANA>

C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; pyroglutamic acid; skin; tachykinin
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 32.3%; Score 20; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
| |||
Db 4 PNAFYGL 10

RESULT 16

I52708

ELAV-like neuronal protein 1, truncated splice form - human

N;Alternate names: Drosophila ELAV(embryonic lethal, abnormal vision)-like 4; Hu antigen D; paraneoplastic encephalomyelitis antigen

C;Species: Homo sapiens (man)

C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000

C;Accession: I52708

R;Sekido, Y.; Bader, S.A.; Carbone, D.P.; Johnson, B.E.; Minna, J.D.
Cancer Res. 54, 4988-4992, 1994

A;Title: Molecular analysis of the HuD gene encoding a paraneoplastic encephalomyelitis antigen in human lung cancer cell lines.

A;Reference number: I52708; MUID:94349312; PMID:8069866

A;Accession: I52708

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-11 <SEK>

A;Cross-references: GB:S73887; NID:g688242; PIDN:AAD14142.1; PID:g4261842

C;Comment: This abnormal peptide is expressed. For the long splice form, see PIR:I38726.

C;Genetics:

A;Gene: GDB:ELAVL4; HUD; PNEM

A;Cross-references: GDB:141875; OMIM:168360

A;Map position: 1p36-1p36

C;Keywords: alternative splicing

Query Match 32.3%; Score 20; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPQNFYKL 8
|| ||
Db 3 MPSRILKL 10

RESULT 17

S07436

tachykinin - African tree frog (Kassina maculata)

N;Alternate names: hylambatin

C;Species: Kassina maculata

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Sep-2000

C;Accession: S07436

R;Yasuhara, T.; Nakajima, T.; Erspamer, G.F.; Erspamer, V.

Biomed. Res. 2, 613-617, 1981

A;Title: New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and hylambatin, in the skin of the African rhacophorid frog Hylambates maculatus.

A;Reference number: S07436

A;Accession: S07436

A;Molecule type: protein

A;Residues: 1-12 <YAS>

A;Experimental source: skin

A;Note: the source is designated as Hylambates maculatus

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;12/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 32.3%; Score 20; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFY 6
| |
Db 5 PDRFY 9

RESULT 18

A09985

gamma-crystallin - haddock (fragments)

C;Species: Melanogrammus aeglefinus (haddock)

C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 18-Jun-1993

C;Accession: A09985

R;Croft, L.R.

Biochim. Biophys. Acta 295, 174-177, 1973

A;Title: Amino and carboxy terminal sequence of gamma-crystallin, from haddock lens.

A;Reference number: A09985; MUID:73088761; PMID:4685070

A;Accession: A09985

A;Molecule type: protein

A;Residues: 1-12 <CRO>

Query Match 32.3%; Score 20; DB 2; Length 12;
Best Local Similarity 42.9%; Pred. No. 1.3e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 FYKLPQM 11
||:: |
Db 5 FYZITDM 11

RESULT 19

S57570

T cell receptor V-J junctional alpha chain region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999

C;Accession: S57570

R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argat, V.P. submitted to the EMBL Data Library, June 1995

A;Description: T cell receptor repertoire for a viral epitope in humans is diversified by tolerance to a background MHC antigen.

A;Reference number: S57494

A;Accession: S57570
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12 <BUR>
A;Cross-references: EMBL:Z49954; NID:g887488; PIDN:CAA90225.1; PID:g887489
C;Keywords: T-cell receptor

Query Match 32.3%; Score 20; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFY 6
| |
Db 6 PNQFY 10

RESULT 20

S74144

aggreCAN - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)

C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999

C;Accession: S74144

R;Bonassar, L.J.; Stinn, J.L.; Paguio, C.G.; Frank, E.H.; Moore, V.L.; Lark, M.W.; Sandy, J.D.; Hollander, A.P.; Poole, A.R.; Grodzinsky, A.J.

Arch. Biochem. Biophys. 333, 359-367, 1996

A;Title: Activation and inhibition of endogenous matrix metalloproteinases in articular cartilage: effects on composition and biophysical properties.

A;Reference number: S74144; MUID:96404934; PMID:8809074

A;Accession: S74144

A;Molecule type: mRNA

A;Residues: 1-12 <BON>

A;Experimental source: cartilage

C;Keywords: cartilage; glycoprotein

Query Match 32.3%; Score 20; DB 2; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.3e+03;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFY 6
:|::|:
Db 4 IPESFF 9

RESULT 21

T37075

hypothetical protein SCJ30.08 - Streptomyces coelicolor

C;Species: Streptomyces coelicolor

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C;Accession: T37075

R;Sanders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1999

A;Reference number: Z21621

A;Accession: T37075

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-16 <SAN>

A;Cross-references: EMBL:AL109973; PIDN:CAB53303.1; GSPDB:GN00070;
SCOEDB:SCJ30.08
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SCJ30.08

Query Match 32.3%; Score 20; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 1.7e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPQNFYKLP 9
||:: ||
Db 7 MPRSAIGLP 15

RESULT 22
C39398

Fc mu (IgM) receptor surface complex gamma chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 20-Mar-1998
C;Accession: C39398
R;Campbell, K.S.; Hager, E.J.; Friedrich, R.J.; Cambier, J.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 3982-3986, 1991
A;Title: IgM antigen receptor complex contains phosphoprotein products of B29
and mb-1 genes.
A;Reference number: A39398; MUID:91219496; PMID:2023945
A;Accession: C39398
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <CAM>

Query Match 30.6%; Score 19; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPQNF 5
:| ||
Db 4 LPLNF 8

RESULT 23
S23306

substance P - Atlantic cod
C;Species: Gadus morhua (Atlantic cod)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
C;Accession: S23306
R;Jensen, J.; Conlon, J.M.
Eur. J. Biochem. 206, 659-664, 1992
A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of
the cod and trout.
A;Reference number: S23186; MUID:92298992; PMID:1376687
A;Accession: S23306
A;Molecule type: protein
A;Residues: 1-11 <JEN>
A;Experimental source: brain
C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gastrointestinal functions
A;Note: substance P is derived by post-translational processing of preprotachykinin A
C;Superfamily: unassigned animal peptides
C;Keywords: neuropeptide; amidated carboxyl end; tachykinin
F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 30.6%; Score 19; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
|| | |
Db 4 PQQFIGL 10

RESULT 24

S23373

T-cell receptor alpha chain J region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

C;Accession: S23373

R;Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichmann, K.; Krawinkel, U.

Eur. J. Immunol. 21, 2749-2754, 1991

A;Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rheumatoid arthritis patients.

A;Reference number: S23364; MUID:92037820; PMID:1657615

A;Accession: S23373

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-11 <PLU>

A;Cross-references: EMBL:X58168

C;Keywords: T-cell receptor

Query Match 30.6%; Score 19; DB 2; Length 11;
Best Local Similarity 42.9%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
| |: |:
Db 3 PSNYDKV 9

RESULT 25

S47358

T-cell antigen receptor VJ junction beta chain - human

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C;Accession: S47358

R;Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T cells bearing the Vb17 gene.

A;Reference number: S47355

A;Accession: S47358

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <LEH>
A;Cross-references: EMBL:Z35682; NID:g527453; PIDN:CAA84751.1; PID:g527454
C;Keywords: T-cell receptor

Query Match 30.6%; Score 19; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQNF 5
||:|
Db 10 PQHF 13

RESULT 26

PA0008

lectin B2 - Psophocarpus scandens (fragment)

C;Species: Psophocarpus scandens

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Mar-1995

C;Accession: PA0008

R;Kortt, A.A.

Phytochemistry 27, 2847-2855, 1988

A;Title: Isolation and characterization of the lectins from the seeds of Psophocarpus scandens.

A;Reference number: PA0005

A;Accession: PA0008

A;Molecule type: protein

A;Residues: 1-15 <KOR>

A;Experimental source: seed

C;Comment: The seeds of Psophocarpus contain two distinct groups of lectins which can be distinguished on the basis of isoelectric point, erythrocyte specificity, and carbohydrate-binding specificity.

C;Keywords: lectin

Query Match 30.6%; Score 19; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 NFYKLPQ 10
|| | |
Db 7 NFNKFEQ 13

RESULT 27

A36279

chemoattractant protein - earthworm (Lumbricus terrestris) (fragment)

C;Species: Lumbricus terrestris (common earthworm)

C;Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 30-Sep-1993

C;Accession: A36279

R;Jiang, X.C.; Inouchi, J.; Wang, D.; Halpern, M.

J. Biol. Chem. 265, 8736-8744, 1990

A;Title: Purification and characterization of a chemoattractant from electric shock-induced earthworm secretion, its receptor binding, and signal transduction through the vomeronasal system of garter snakes.

A;Reference number: A36279; MUID:90256800; PMID:2160465

A;Accession: A36279

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <JIA>

Query Match 30.6%; Score 19; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PQNFYKLP 9
| | ||
Db 5 PPGFTYLP 12

RESULT 28

S51735

T-cell receptor beta-chain joining region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 05-Nov-1999

C;Accession: S51735

R;Durinovic-Bello, I.; Steinle, A.; Ziegler, A.G.; Schendel, D.J.

submitted to the EMBL Data Library, November 1993

A;Reference number: S51732

A;Accession: S51735

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-15 <DUR>

A;Cross-references: EMBL:Z28344; NID:g607122; PIDN:CAA82198.1; PID:g607123

C;Keywords: T-cell receptor

Query Match 30.6%; Score 19; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQNF 5
||:|
Db 12 PQHF 15

RESULT 29

B49655

T-cell-receptor beta chain variable region, TCR V beta (clone SF-2) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997

C;Accession: B49655

R;Grom, A.A.; Thompson, S.D.; Luyrink, L.; Passo, M.; Choi, E.; Glass, D.N.

Proc. Natl. Acad. Sci. U.S.A. 90, 11104-11108, 1993

A;Title: Dominant T-cell-receptor beta chain variable region V beta 14+ clones in juvenile rheumatoid arthritis.

A;Reference number: A49655; MUID:94068553; PMID:8248215

A;Accession: B49655

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-15 <GRO>

A;Experimental source: knee joint, synovial fluid lymphocytes

A;Note: sequence extracted from NCBI backbone (NCBIP:140446)

C;Keywords: T-cell receptor

Query Match 30.6%; Score 19; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQNF 5
||:|
Db 11 PQHF 14

RESULT 30

S22040

cob protein - common sunflower

C;Species: Helianthus annuus (common sunflower)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Sep-1997

C;Accession: S22040

R;Koehler, R.H.

submitted to the EMBL Data Library, October 1991

A;Reference number: S22040

A;Accession: S22040

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-16 <KOE>

A;Cross-references: EMBL:X62592; NID:g12990; PID:g12991

Query Match 30.6%; Score 19; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NFY 6
|||
Db 3 NFY 5

RESULT 31

PH1778

T cell receptor alpha chain V region (clone 1PBL V alpha 24-5) - human
(fragment)

C;Species: Homo sapiens (man)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C;Accession: PH1778

R;Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A;Title: Analysis of T cell antigen receptor (TCR) expression by human
peripheral blood CD4-8-alpha/beta T cells demonstrates preferential use of
several V beta genes and an invariant TCR alpha chain.

A;Reference number: PH1754; MUID:93301585; PMID:8391057

A;Accession: PH1778

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-16 <POR>

Query Match 30.6%; Score 19; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NFYKL 8

| | | |
Db 10 NDYKL 14

RESULT 32

E49255

T-cell receptor beta chain V-D-J-C region (V beta 17, J beta 1.5) - human
(fragment)

C;Species: Homo sapiens (man)

C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997

C;Accession: E49255

R;Rosenberg, W.M.; Moss, P.A.; Bell, J.I.

Eur. J. Immunol. 22, 541-549, 1992

A;Title: Variation in human T cell receptor V beta and J beta repertoire:
analysis using anchor polymerase chain reaction.

A;Reference number: A49039; MUID:92164737; PMID:1311263

A;Accession: E49255

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-16 <ROS>

A;Note: sequence extracted from NCBI backbone (NCBIP:90726)

C;Keywords: T-cell receptor

Query Match 30.6%; Score 19; DB 2; Length 16;
Best Local Similarity 75.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQNF 5
 | | : |
Db 12 PQHF 15

RESULT 33

F49039

T-cell receptor beta chain V-D-J-C region (V beta 2, J beta 1.5) - human
(fragment)

C;Species: Homo sapiens (man)

C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997

C;Accession: F49039

R;Rosenberg, W.M.; Moss, P.A.; Bell, J.I.

Eur. J. Immunol. 22, 541-549, 1992

A;Title: Variation in human T cell receptor V beta and J beta repertoire:
analysis using anchor polymerase chain reaction.

A;Reference number: A49039; MUID:92164737; PMID:1311263

A;Accession: F49039

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-16 <ROS>

A;Note: sequence extracted from NCBI backbone (NCBIP:90718)

C;Keywords: T-cell receptor

Query Match 30.6%; Score 19; DB 2; Length 16;
Best Local Similarity 75.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQNF 5
 | | : |

Db 12 PQHF 15

RESULT 34

S23971

alpha-macroglobulin proteinase inhibitor - common octopus

C;Species: Octopus vulgaris (common octopus)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C;Accession: S23971

R;Thogersen, I.B.; Salvesen, G.; Brucato, F.H.; Pizzo, S.V.; Enghild, J.J.

Biochem. J. 285, 521-527, 1992

A;Title: Purification and characterization of an alpha-macroglobulin proteinase inhibitor from the mollusc Octopus vulgaris.

A;Reference number: S23971; MUID:92344633; PMID:1379044

A;Accession: S23971

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-18 <THO>

Query Match 30.6%; Score 19; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NFY 6
|||
Db 12 NFY 14

RESULT 35

B24749

neuropeptide B - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 18-Aug-2000

C;Accession: B24749

R;Yang, H.Y.T.; Fratta, W.; Majane, E.A.; Costa, E.

Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985

A;Title: Isolation, sequencing, synthesis, and pharmacological characterization of two brain neuropeptides that modulate the action of morphine.

A;Reference number: A94074; MUID:86067985; PMID:3865193

A;Accession: B24749

A;Molecule type: protein

A;Residues: 1-8 <YAN>

C;Superfamily: unassigned animal peptides

C;Keywords: neuropeptide

Query Match 29.0%; Score 18; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PQNF 5
|||
Db 5 PQRF 8

RESULT 36

I49404

prealbumin - western wild mouse (fragment)

C;Species: Mus spretus (western wild mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: I49404
R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.;
Nadeau, J.H.
Mamm. Genome 5, 349-355, 1994
A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A;Reference number: I48934; MUID:94319082; PMID:8043949
A;Accession: I49404
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-8 <RES>
A;Cross-references: EMBL:U05689; NID:g497008; PIDN:AAB60461.1; PID:g642825

Query Match 29.0%; Score 18; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQN 4
| | |
Db 6 PQN 8

RESULT 37

F60409

substance P-like peptide II - frog (Pseudophryne guentheri)

C;Species: Pseudophryne guentheri

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000

C;Accession: F60409

R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;
Melchiorri, P.; Erspamer, V.

Peptides 11, 299-304, 1990

A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of
the Australian frog Pseudophryne guentheri.

A;Reference number: A60409; MUID:90287814; PMID:2356157

A;Accession: F60409

A;Molecule type: protein

A;Residues: 1-11 <SIM>

C;Superfamily: unassigned animal peptides

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 29.0%; Score 18; DB 2; Length 11;
Best Local Similarity 42.9%; Pred. No. 2.8e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
| | : |
Db 4 PNEFFGL 10

RESULT 38

E60409

substance P-like peptide I - frog (Pseudophryne guentheri)

C;Species: Pseudophryne guentheri

C;Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 02-Sep-2000

C;Accession: E60409
R;Simmaco, M.; Severini, C.; De Biase, D.; Barra, D.; Bossa, F.; Roberts, J.D.;
Melchiorri, P.; Erspamer, V.
Peptides 11, 299-304, 1990
A;Title: Six novel tachykinin- and bombesin-related peptides from the skin of
the Australian frog *Pseudophryne guentheri*.
A;Reference number: A60409; MUID:90287814; PMID:2356157
A;Accession: E60409
A;Molecule type: protein
A;Residues: 1-11 <SIM>
C;Superfamily: unassigned animal peptides
C;Keywords: amidated carboxyl end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 29.0%; Score 18; DB 2; Length 11;
Best Local Similarity 42.9%; Pred. No. 2.8e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
| |:
Db 4 PDEFFGL 10

RESULT 39

S23308

substance P - rainbow trout

C;Species: *Oncorhynchus mykiss* (rainbow trout)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000

C;Accession: S23308

R;Jensen, J.; Conlon, J.M.

Eur. J. Biochem. 206, 659-664, 1992

A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of
the cod and trout.

A;Reference number: S23186; MUID:92298992; PMID:1376687

A;Accession: S23308

A;Molecule type: protein

A;Residues: 1-11 <JEN>

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular
and gastrointestinal functions

A;Note: substance P is derived by post-translational processing of
preprotachykinin A

C;Superfamily: unassigned animal peptides

C;Keywords: neuropeptide; amidated carboxyl end; tachykinin

F;11/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 29.0%; Score 18; DB 2; Length 11;
Best Local Similarity 42.9%; Pred. No. 2.8e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
| |:
Db 4 PHQFFGL 10

RESULT 40

S01119

photosystem II protein psbK - spinach chloroplast (fragment)

C;Species: chloroplast *Spinacia oleracea* (spinach)

C;Date: 30-Jun-1989 #sequence_revision 31-Dec-1990 #text_change 19-Jan-1996

C;Accession: S01119

R;Murata, N.; Miyao, M.; Hayashida, N.; Hidaka, T.; Sugiura, M.

FEBS Lett. 235, 283-288, 1988

A;Title: Identification of a new gene in the chloroplast genome encoding a low-molecular-mass polypeptide of photosystem II complex.

A;Reference number: S01119

A;Accession: S01119

A;Molecule type: protein

A;Residues: 1-13 <MUR>

C;Genetics:

A;Gene: psbK

A;Genome: chloroplast

C;Superfamily: photosystem II protein psbK

C;Keywords: chloroplast; membrane-associated complex; photosynthesis; photosystem II; thylakoid

Query Match 29.0%; Score 18; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KLPQ 10
|||:
Db 1 KLPE 4

RESULT 41

I70076

glycophorin B/glycophorin A mutant fusion protein St-a (mistranslated) - human (fragment)

C;Species: *Homo sapiens* (man)

C;Date: 24-May-1996 #sequence_revision 14-Aug-1997 #text_change 20-Apr-2000

C;Accession: I70076

R;Rearden, A.; Phan, H.; Dubnicoff, T.; Kudo, S.; Fukuda, M.

J. Biol. Chem. 265, 9259-9263, 1990

A;Title: Identification of the crossing-over point of a hybrid gene encoding human glycophorin variant St-a: Similarity to the crossing-over point in haptoglobin-related genes.

A;Reference number: I55334; MUID:90264417; PMID:1971625

A;Accession: I70076

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-13 <REA>

A;Cross-references: GB:M33507; GB:J05465; NID:g183743; PIDN:AAA35942.1;

PID:g442426

A;Note: the translation is from an incorrect reading frame

C;Genetics:

A;Gene: GYPB/GYPA

C;Keywords: fusion protein

Query Match 29.0%; Score 18; DB 4; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 YKLP 9
| |
Db 4 YNLP 7

RESULT 42

B36079

hypothetical protein insulin-like growth factor I 5'-region - African clawed frog

C;Species: *Xenopus laevis* (African clawed frog)

C;Date: 30-Nov-1990 #sequence_revision 13-Sep-1991 #text_change 18-Aug-2000

C;Accession: B36079

R;Kajimoto, Y.; Rotwein, P.

Mol. Endocrinol. 4, 217-226, 1990

A;Title: Evolution of insulin-like growth factor I (IGF-I): structure and expression of an IGF-I precursor from *Xenopus laevis*.

A;Reference number: A36079; MUID:90231335; PMID:2330002

A;Accession: B36079

A;Molecule type: mRNA

A;Residues: 1-14 <KAJ>

A;Cross-references: GB:M29857; NID:g214287; PIDN:AAA70329.1; PID:g903887

A;Note: the authors translated the codon CAG for residue 4 as Gly

C;Superfamily: unassigned leader peptides

Query Match 29.0%; Score 18; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPQM 11
| | | :
Db 2 LPQL 5

RESULT 43

S58862

botulinum neurotoxin type A and B hemagglutinin component II - *Clostridium botulinum* (strain NCTC 7272) (fragment)

N;Alternate names: HA-II protein

C;Species: *Clostridium botulinum*

C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 15-Oct-1999

C;Accession: S58862; S58858

R;East, A.K.; Stacey, J.M.; Collins, M.D.

Syst. Appl. Microbiol. 17, 306-312, 1994

A;Title: Cloning and sequencing of a hemagglutinin component of the botulinum neurotoxin complex encoded by *Clostridium botulinum* types A and B.

A;Reference number: S58855

A;Accession: S58862

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-14 <EAS>

A;Cross-references: EMBL:X79104; NID:g870937; PIDN:CAA55719.1; PID:g870941

A;Experimental source: strain NCTC 7272

A;Accession: S58858

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-14 <EA2>

A;Cross-references: EMBL:X79103; NID:g870932; PIDN:CAA55715.1; PID:g870936
A;Experimental source: strain Eklund 17B
C;Keywords: hemagglutinin; neurotoxin

Query Match 29.0%; Score 18; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 3.6e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPQNFYK 7
:| ||
Db 8 LPNGNYK 14

RESULT 44

S58866

botulinum neurotoxin type B hemagglutinin component II - Clostridium botulinum
(NCTC 7273) (fragment)

N;Alternate names: protein HA-II

C;Species: Clostridium botulinum

A;Variety: NCTC 7273

C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 15-Oct-1999

C;Accession: S58866

R;East, A.K.; Stacey, J.M.; Collins, M.D.

Syst. Appl. Microbiol. 17, 306-312, 1994

A;Title: Cloning and sequencing of a hemagglutinin component of the botulinum
neurotoxin complex encoded by Clostridium botulinum types A and B.

A;Reference number: S58855

A;Accession: S58866

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-14 <EAS>

A;Cross-references: EMBL:X79102; NID:g870942; PIDN:CAA55711.1; PID:g870946

A;Experimental source: NCTC 7273

C;Keywords: hemagglutinin; neurotoxin

Query Match 29.0%; Score 18; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 3.6e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPQNFYK 7
:| ||
Db 8 LPNGNYK 14

RESULT 45

PL0152

metal-binding protein - reticulate nassa (fragment)

C;Species: Nassarius reticulatus (reticulate nassa)

C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 20-Jun-2000

C;Accession: PL0152

R;Andersen, R.A.; Eriksen, K.D.H.; Bakke, T.

Comp. Biochem. Physiol. B 94, 285-291, 1989

A;Title: Evidence of presence of a low molecular weight, non-metalllothionein-
like metal-binding protein in the marine gastropod Nassarius reticulatus L.

A;Reference number: PL0152

A;Accession: PL0152

A;Molecule type: protein

A;Residues: 1-14 <AND>

C;Comment: This protein is induced in environments contaminated with heavy metal.

Query Match 29.0%; Score 18; DB 2; Length 14;
Best Local Similarity 37.5%; Pred. No. 3.6e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPQNFYKL 8
:|: | |
Db 5 VPREXYPL 12

RESULT 46

B20872

alpha-2-macroglobulin - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000

C;Accession: B20872

R;Nagase, H.; Harris Jr., E.D.; Woessner Jr., J.F.; Brew, K.

J. Biol. Chem. 258, 7481-7489, 1983

A;Title: Ovostatin: a novel proteinase inhibitor from chicken egg white. I. Purification, physicochemical properties, and tissue distribution of ovostatin.

A;Reference number: A92427; MUID:83238315; PMID:6408074

A;Accession: B20872

A;Molecule type: protein

A;Residues: 1-14 <NAG>

Query Match 29.0%; Score 18; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PQNFYKLP 9
|| ||
Db 6 PQYMVLLP 13

RESULT 47

PT0294

Ig heavy chain CRD3 region (clone 4-133) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0294

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G. J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and joining segments in adult human peripheral blood B lymphocytes.

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0294

A;Molecule type: DNA

A;Residues: 1-14 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match 29.0%; Score 18; DB 2; Length 14;
Best Local Similarity 37.5%; Pred. No. 3.6e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PQNFKLP 9
|::| |
Db 6 PRDGYDTP 13

RESULT 48

S08209

hypothetical protein 2 - garden pea

N;Alternate names: phytochrome

C;Species: Pisum sativum (garden pea)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Sep-1997

C;Accession: S08209

R;Sato, N.

Plant Mol. Biol. 11, 697-710, 1988

A;Title: Nucleotide sequence and expression of the phytochrome gene in Pisum sativum: differential regulation by light of multiple transcripts.

A;Reference number: S06856

A;Accession: S08209

A;Molecule type: DNA

A;Residues: 1-15 <SAT>

A;Cross-references: EMBL:X14077; NID:g20836; PID:g20838

C;Genetics:

A;Gene: phy

Query Match 29.0%; Score 18; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.8e+03;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 PQNFKLPQM 11
| | | | :
Db 6 PTNGYFNPYL 15

RESULT 49

A56049

urinary tract stone matrix protein, 40K - unidentified organism (fragment)

C;Species: unidentified organism

C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 20-Apr-2000

C;Accession: A56049

R;Binette, J.P.; Binette, M.B.

Scanning Microsc. 8, 233-239, 1994

A;Title: Sequencing of proteins extracted from stones.

A;Reference number: A56049; MUID:95215817; PMID:7701298

A;Accession: A56049

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <BIN>

A;Experimental source: urinary tract and gallbladder stones

A;Note: the source is designated as Homo sapiens, however the true source probably originates in infectious contamination (see PIR:S00157)

Query Match 29.0%; Score 18; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 3.8e+03;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MPQNFY 6

Db :|: |
 9 LPEKLY 14

RESULT 50

I38335

hypothetical TEL/MN1 mutant fusion protein type II - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000

C;Accession: I38335

R;Buijs, A.; Sherr, S.; van Baal, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A.G.; Riegman, P.; Lekanne Deprez, R.; Zwarthoff, E.; Hagemeijer, A.; Grosveld, G.

Oncogene 10, 1511-1519, 1995

A;Title: Translocation (12;22) (p13;q11) in myeloproliferative disorders results in fusion of the ETS-like TEL gene on 12p13 to the MN1 gene on 22q11.

A;Reference number: I38031; MUID:95249265; PMID:7731705

A;Accession: I38335

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-15 <BUI>

A;Cross-references: EMBL:X85024; NID:g971471; PIDN:CAA59397.1; PID:g971472

C;Comment: This sequence is the chimeric product of a translocation mutation.

C;Genetics:

A;Gene: ETV6/MN1; TEL/MN1

A;Map position: 22q11/12p13

C;Keywords: fusion protein

Query Match 29.0%; Score 18; DB 4; Length 15;
Best Local Similarity 37.5%; Pred. No. 3.8e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PQNFYKLP 9
 | : : ||
Db 5 PHSADLP 12

Search completed: July 4, 2004, 04:47:18
Job time : 9.45522 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 4, 2004, 04:45:52 ; Search time 21.5896 Seconds
(without alignments)
158.601 Million cell updates/sec

Title: US-09-641-802-6
Perfect score: 62
Sequence: 1 MPQNFYKLPQM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 203405

Minimum DB seq length: 7
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

%
Result Query
No. Score Match Length DB ID Description

1	62	100.0	11	14	US-10-281-652-6	Sequence 6, Appli
2	29	46.8	7	12	US-09-889-468-54	Sequence 54, Appl
3	29	46.8	10	14	US-10-062-710-83	Sequence 83, Appl
4	29	46.8	15	9	US-09-888-721-10	Sequence 10, Appl
5	28	45.2	12	12	US-10-432-585-3	Sequence 3, Appli
6	28	45.2	12	14	US-10-075-869-41	Sequence 41, Appl
7	28	45.2	12	15	US-10-366-493-41	Sequence 41, Appl
8	28	45.2	18	10	US-09-852-370-31	Sequence 31, Appl
9	28	45.2	18	14	US-10-002-244-4	Sequence 4, Appli
10	26	41.9	9	12	US-10-014-340-803	Sequence 803, App
11	26	41.9	11	9	US-09-920-174-3	Sequence 3, Appli
12	26	41.9	11	10	US-09-920-195A-3	Sequence 3, Appli
13	26	41.9	15	14	US-10-125-869A-43	Sequence 43, Appl
14	26	41.9	15	14	US-10-125-869A-119	Sequence 119, App
15	26	41.9	15	15	US-10-462-262-267	Sequence 267, App
16	26	41.9	15	15	US-10-462-262-343	Sequence 343, App
17	26	41.9	16	9	US-09-799-576A-22	Sequence 22, Appl
18	26	41.9	16	9	US-09-799-540-22	Sequence 22, Appl
19	26	41.9	16	9	US-09-799-608-22	Sequence 22, Appl
20	26	41.9	16	10	US-09-798-932-22	Sequence 22, Appl
21	26	41.9	16	12	US-09-799-680-22	Sequence 22, Appl
22	26	41.9	17	10	US-09-745-078A-21	Sequence 21, Appl
23	26	41.9	17	10	US-09-962-756-1205	Sequence 1205, Ap
24	26	41.9	17	10	US-09-962-756-1757	Sequence 1757, Ap
25	26	41.9	17	10	US-09-962-756-1911	Sequence 1911, Ap
26	26	41.9	17	14	US-10-374-624-21	Sequence 21, Appl
27	26	41.9	17	15	US-10-253-471-1205	Sequence 1205, Ap
28	26	41.9	17	15	US-10-253-471-1757	Sequence 1757, Ap
29	26	41.9	17	15	US-10-253-471-1911	Sequence 1911, Ap
30	26	41.9	17	16	US-10-253-493-1205	Sequence 1205, Ap
31	26	41.9	17	16	US-10-253-493-1757	Sequence 1757, Ap
32	26	41.9	17	16	US-10-253-493-1911	Sequence 1911, Ap
33	26	41.9	18	10	US-09-745-078A-20	Sequence 20, Appl
34	26	41.9	18	14	US-10-374-624-20	Sequence 20, Appl
35	25	40.3	8	9	US-09-756-283A-42	Sequence 42, Appl
36	25	40.3	8	9	US-09-756-283A-58	Sequence 58, Appl
37	25	40.3	8	9	US-09-756-283A-69	Sequence 69, Appl
38	25	40.3	8	9	US-09-756-283A-90	Sequence 90, Appl
39	25	40.3	8	9	US-09-756-283A-96	Sequence 96, Appl
40	25	40.3	8	13	US-10-078-968-2	Sequence 2, Appli
41	25	40.3	9	12	US-10-253-286-107	Sequence 107, App
42	25	40.3	9	15	US-10-245-871-107	Sequence 107, App
43	25	40.3	10	13	US-10-007-761-41	Sequence 41, Appl
44	25	40.3	11	12	US-10-343-654-27	Sequence 27, Appl
45	25	40.3	11	14	US-10-119-528-31	Sequence 31, Appl
46	25	40.3	12	9	US-09-813-653-27	Sequence 27, Appl
47	25	40.3	12	9	US-09-865-018-10	Sequence 10, Appl
48	25	40.3	12	10	US-09-845-612B-10	Sequence 10, Appl
49	25	40.3	14	12	US-10-253-286-120	Sequence 120, App
50	25	40.3	14	15	US-10-245-871-120	Sequence 120, App
51	25	40.3	15	14	US-10-254-763-1	Sequence 1, Appli
52	25	40.3	18	9	US-09-864-761-36589	Sequence 36589, A
53	24.5	39.5	15	14	US-10-239-313A-518	Sequence 518, App
54	24	38.7	7	11	US-09-261-894-69	Sequence 69, Appl
55	24	38.7	8	15	US-10-408-133-26	Sequence 26, Appl
56	24	38.7	9	8	US-08-344-824-331	Sequence 331, App

57	24	38.7	9	9	US-09-835-948-73	Sequence 73, Appl
58	24	38.7	9	9	US-09-835-948-101	Sequence 101, App
59	24	38.7	9	12	US-09-749-831-6	Sequence 6, Appli
60	24	38.7	9	14	US-10-223-047-27	Sequence 27, Appl
61	24	38.7	9	14	US-10-172-597-73	Sequence 73, Appl
62	24	38.7	9	14	US-10-172-597-101	Sequence 101, App
63	24	38.7	9	15	US-10-428-335-92	Sequence 92, Appl
64	24	38.7	9	15	US-10-428-335-133	Sequence 133, App
65	24	38.7	10	8	US-08-344-824-214	Sequence 214, App
66	24	38.7	11	14	US-10-105-232-495	Sequence 495, App
67	24	38.7	11	14	US-10-189-437-482	Sequence 482, App
68	24	38.7	12	10	US-09-880-748-2884	Sequence 2884, Ap
69	24	38.7	12	12	US-10-293-418-2884	Sequence 2884, Ap
70	24	38.7	12	15	US-10-360-522-6	Sequence 6, Appli
71	24	38.7	13	10	US-09-927-734C-10	Sequence 10, Appl
72	24	38.7	13	16	US-10-264-309-176	Sequence 176, App
73	24	38.7	14	15	US-10-350-367-7	Sequence 7, Appli
74	24	38.7	15	10	US-09-983-802-539	Sequence 539, App
75	24	38.7	15	12	US-09-973-278-631	Sequence 631, App
76	24	38.7	15	12	US-09-984-490-539	Sequence 539, App
77	24	38.7	15	14	US-10-208-349-10	Sequence 10, Appl
78	24	38.7	16	14	US-10-096-986-17	Sequence 17, Appl
79	24	38.7	16	15	US-10-350-405-20	Sequence 20, Appl
80	24	38.7	17	8	US-08-979-847-38	Sequence 38, Appl
81	24	38.7	17	14	US-10-225-567A-1486	Sequence 1486, Ap
82	24	38.7	17	14	US-10-105-232-441	Sequence 441, App
83	24	38.7	17	14	US-10-105-232-494	Sequence 494, App
84	24	38.7	17	14	US-10-430-442-42	Sequence 42, Appl
85	24	38.7	17	14	US-10-189-437-428	Sequence 428, App
86	24	38.7	17	14	US-10-189-437-481	Sequence 481, App
87	24	38.7	17	14	US-10-114-104-38	Sequence 38, Appl
88	24	38.7	18	10	US-09-932-613-92	Sequence 92, Appl
89	24	38.7	18	10	US-09-932-322-92	Sequence 92, Appl
90	24	38.7	18	14	US-10-084-813-272	Sequence 272, App
91	24	38.7	18	14	US-10-084-813-273	Sequence 273, App
92	24	38.7	18	14	US-10-084-813-274	Sequence 274, App
93	24	38.7	18	14	US-10-084-813-275	Sequence 275, App
94	23.5	37.9	9	8	US-08-452-843A-6	Sequence 6, Appli
95	23	37.1	8	9	US-09-756-283A-70	Sequence 70, Appl
96	23	37.1	8	11	US-09-943-944E-175	Sequence 175, App
97	23	37.1	9	9	US-09-835-948-149	Sequence 149, App
98	23	37.1	9	9	US-09-835-948-159	Sequence 159, App
99	23	37.1	9	9	US-09-909-460-101	Sequence 101, App
100	23	37.1	9	9	US-09-972-772-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
 US-10-281-652-6
 ; Sequence 6, Application US/10281652
 ; Publication No. US20030091606A1
 ; GENERAL INFORMATION:
 ; APPLICANT: STANTON, G. John
 ; APPLICANT: HUGHES, Thomas K.
 ; APPLICANT: BOLDOGH, Istvan

; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265.00220101
; CURRENT APPLICATION NUMBER: US/10/281,652
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US/09/641,803
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-281-652-6

Query Match 100.0%; Score 62; DB 14; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFYKLPQM 11
| | | | | | | | | |
Db 1 MPQNFYKLPQM 11

RESULT 2

US-09-889-468-54

; Sequence 54, Application US/09889468
; Publication No. US20020125674A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pasteur Limited
; TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and
uses thereof
; FILE REFERENCE: 77813-86
; CURRENT APPLICATION NUMBER: US/09/889,468
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/113,280
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,281
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,282
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,283
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,284
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,285
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113,385
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114,050
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 60/114,056

; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: 60/114,057
; PRIOR FILING DATE: 1998-12-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: B-cell epitope from SEQ ID NO:26
US-09-889-468-54

Query Match 46.8%; Score 29; DB 12; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QNFYK 7
| | | |
Db 1 QNFYK 5

RESULT 3

US-10-062-710-83

; Sequence 83, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; TITLE OF INVENTION: Via Peptide Vaccines
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV CTL-Epitopes
US-10-062-710-83

Query Match 46.8%; Score 29; DB 14; Length 10;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
| | | |
Db 1 PDRFYKL 7

RESULT 4

US-09-888-721-10

; Sequence 10, Application US/09888721
 ; Patent No. US20020132990A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Huston, James S.
 ; APPLICANT: Wils, Pierre
 ; APPLICANT: Zhu, Quan
 ; APPLICANT: Laurent, Olivier
 ; APPLICANT: Marasco, Wayne A.
 ; APPLICANT: Scherman, Daniel
 ; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
 ; TITLE OF INVENTION: DELIVERY
 ; FILE REFERENCE: 23611-A USA
 ; CURRENT APPLICATION NUMBER: US/09/888,721
 ; CURRENT FILING DATE: 2001-06-25
 ; PRIOR APPLICATION NUMBER: 60/213,653
 ; PRIOR FILING DATE: 2000-06-23
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Epstein-Barr Virus

US-09-888-721-10

Query Match 46.8%; Score 29; DB 9; Length 15;
 Best Local Similarity 50.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PQNFYKLPQM 11
 | || :| |
 Db 4 PTVFYNIPPM 13

RESULT 5

US-10-432-585-3

; Sequence 3, Application US/10432585
 ; Publication No. US20040029215A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUENAGA, Masato
 ; APPLICANT: YAMADA, Takao
 ; APPLICANT: NISHIMURA, Osamu
 ; TITLE OF INVENTION: Method of Production for RFRP
 ; FILE REFERENCE: 2829 USOP
 ; CURRENT APPLICATION NUMBER: US/10/432,585
 ; CURRENT FILING DATE: 2003-05-23
 ; PRIOR APPLICATION NUMBER: JP 2000-373125
 ; PRIOR FILING DATE: 2000-12-07
 ; NUMBER OF SEQ ID NOS: 30
 ; SEQ ID NO 3
 ; LENGTH: 12
 ; TYPE: PRT
 ; ORGANISM: Human

US-10-432-585-3

Query Match 45.2%; Score 28; DB 12; Length 12;
Best Local Similarity 55.6%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPQNFYKLP 9
|| :| ||
Db 1 MPHSFANLP 9

RESULT 6

US-10-075-869-41

; Sequence 41, Application US/10075869
; Publication No. US20030104622A1
; GENERAL INFORMATION:
; APPLICANT: Robbins, Paul D.
; APPLICANT: Mi, Zhibao
; APPLICANT: Frizzell, Raymond
; APPLICANT: Glorioso, Joseph C.
; APPLICANT: Gambotto, Andrea
; TITLE OF INVENTION: IDENTIFICATION OF PEPTIDES THAT
; TITLE OF INVENTION: FACILITATE UPTAKE AND CYTOPLASMIC AND/OR NUCLEAR
TRANSPORT
; TITLE OF INVENTION: OF PROTEINS, DNA AND VIRUSES
; FILE REFERENCE: AP32573-AAA 072396.0237
; CURRENT APPLICATION NUMBER: US/10/075,869
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 60/151,980
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: 60/188,944
; PRIOR FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: random peptide library
US-10-075-869-41

Query Match 45.2%; Score 28; DB 14; Length 12;
Best Local Similarity 44.4%; Pred. No. 2.6e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3 QNFYKLPQM 11
:||: ||::
Db 4 KNFFWLPEL 12

RESULT 7

US-10-366-493-41

; Sequence 41, Application US/10366493
; Publication No. US20030219826A1
; GENERAL INFORMATION:
; APPLICANT: Robbins, Paul D.
; APPLICANT: Mi, Zhibao
; APPLICANT: Frizzell, Raymond

```
; APPLICANT:  Glorioso, Joseph C.
; APPLICANT:  Gambotto, Andrea
; APPLICANT:  Mai, Jeffrey C.
; TITLE OF INVENTION:  IDENTIFICATION OF PEPTIDES THAT FACILITATE UPTAKE AND
CYTOPLASMIC AND /OR
; TITLE OF INVENTION:  NUCLEAR TRANSPORT
; TITLE OF INVENTION:  OF PROTEINS, DNA AND VIRUSES
; FILE REFERENCE:  AP32573-A-A-A-A 072396.0246
; CURRENT APPLICATION NUMBER:  US/10/366,493
; CURRENT FILING DATE:  2003-02-12
; PRIOR APPLICATION NUMBER:  10/075,869
; PRIOR FILING DATE:  2002-02-13
; PRIOR APPLICATION NUMBER:  09/653,182
; PRIOR FILING DATE:  2000-08-31
; PRIOR APPLICATION NUMBER:  60/188,944
; PRIOR FILING DATE:  2000-03-13
; PRIOR APPLICATION NUMBER:  60/151,980
; PRIOR FILING DATE:  1999-09-01
; NUMBER OF SEQ ID NOS:  107
; SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 41
;   LENGTH:  12
;   TYPE:  PRT
;   ORGANISM:  Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION:  pep 35
US-10-366-493-41
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Query Match          45.2%;  Score 28;  DB 15;  Length 12;
Best Local Similarity  44.4%;  Pred. No. 2.6e+02;
Matches      4;  Conservative      4;  Mismatches      1;  Indels      0;  Gaps      0;
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```
Qy      3 QNFYKLPQM 11
        :||: ||::
Db      4 KNFFWLPEL 12
```

RESULT 8

US-09-852-370-31

```
; Sequence 31, Application US/09852370
; Publication No. US20030126624A1
; GENERAL INFORMATION:
; APPLICANT:  Pomerantz, Joel L.
; APPLICANT:  Sharp, Phillip A.
; APPLICANT:  Pabo, Carl O.
; TITLE OF INVENTION:  Chimeric DNA-binding proteins
; FILE REFERENCE:  APV-022.02
; CURRENT APPLICATION NUMBER:  US/09/852,370
; CURRENT FILING DATE:  2001-05-10
; PRIOR APPLICATION NUMBER:  08/973,131
; PRIOR FILING DATE:  1997-11-26
; PRIOR APPLICATION NUMBER:  PCT/US95/16982
; PRIOR FILING DATE:  1995-12-29
; PRIOR APPLICATION NUMBER:  08/366,083
; PRIOR FILING DATE:  1994-12-29
; NUMBER OF SEQ ID NOS:  75
; SOFTWARE:  PatentIn Ver. 2.0
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; SEQ ID NO 31
; LENGTH: 18
; TYPE: PRT
; ORGANISM: human
US-09-852-370-31

Query Match 45.2%; Score 28; DB 10; Length 18;
Best Local Similarity 71.4%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NFYKLPQ 10
|| :|||
Db 1 NFLQLPQ 7

RESULT 9

US-10-002-244-4
; Sequence 4, Application US/10002244
; Publication No. US20030143731A1
; GENERAL INFORMATION:
; APPLICANT: ARIAD Gene Therapeutics, Inc.
; TITLE OF INVENTION: Use of Heterologous Transcription Factors in Gene Therapy
; FILE REFERENCE: 346B USC1
; CURRENT APPLICATION NUMBER: US/10/002,244
; CURRENT FILING DATE: 2002-01-29
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: homo sapien
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(18)
; OTHER INFORMATION: glutamine rich region of Oct-2
US-10-002-244-4

Query Match 45.2%; Score 28; DB 14; Length 18;
Best Local Similarity 71.4%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NFYKLPQ 10
|| :|||
Db 1 NFLQLPQ 7

RESULT 10

US-10-014-340-803
; Sequence 803, Application US/10014340
; Publication No. US20030064411A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; TITLE OF INVENTION: Diagnosis and Treatment of Alzheimer's Disease
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340

; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 803
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-803

Query Match 41.9%; Score 26; DB 12; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
|:|:|
Db 2 PENFFLL 8

RESULT 11

US-09-920-174-3
; Sequence 3, Application US/09920174
; Patent No. US20020150590A1
; GENERAL INFORMATION:
; APPLICANT: KHANNA, RAJIV
; APPLICANT: KERR, BEVERLEY M.
; APPLICANT: MISKO, IHOR S.
; APPLICANT: MOSS, DENIS J.
; APPLICANT: BURROWS, SCOTT R.
; TITLE OF INVENTION: EBV CTL EPITOPES
; FILE REFERENCE: FBRC:008USC2
; CURRENT APPLICATION NUMBER: US/09/920,174
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/920,175
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/194,450
; PRIOR FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-920-174-3

Query Match 41.9%; Score 26; DB 9; Length 11;
Best Local Similarity 57.1%; Pred. No. 5.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 FYKLPQM 11
||:|
Db 3 FYNIPPM 9

RESULT 12

US-09-920-195A-3

; Sequence 3, Application US/09920195A
; Publication No. US20030175300A1
; GENERAL INFORMATION:
; APPLICANT: KHANNA, RAJIV
; APPLICANT: KERR, BEVERLEY M.
; APPLICANT: MISKO, IHOR S.
; APPLICANT: MOSS, DENIS J.
; APPLICANT: BURROWS, SCOTT R.
; TITLE OF INVENTION: EBV CTL EPITOPES
; FILE REFERENCE: FBRC:008USC1
; CURRENT APPLICATION NUMBER: US/09/920,195A
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 09/194,450
; PRIOR FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide

US-09-920-195A-3

Query Match 41.9%; Score 26; DB 10; Length 11;
Best Local Similarity 57.1%; Pred. No. 5.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 FYKLPQM 11
|| :| |
Db 3 FYNIPPM 9

RESULT 13

US-10-125-869A-43

; Sequence 43, Application US/10125869A
; Publication No. US20030199671A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac Jesus
; APPLICANT: Wu, Qi-Long
; APPLICANT: Ley, Arthur C.
; APPLICANT: Stochl, Mark
; APPLICANT: Ransohoff, Thomas C.
; APPLICANT: Potter, M. Daniel (deceased)
; TITLE OF INVENTION: BINDING MOLECULES FOR Fc-REGION
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 3421.1006-001
; CURRENT APPLICATION NUMBER: US/10/125,869A
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/284,534
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 15

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc region binding polypeptide
US-10-125-869A-43

Query Match 41.9%; Score 26; DB 14; Length 15;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NFYKLP 9
||::||
Db 5 NFWQLP 10

RESULT 14

US-10-125-869A-119

; Sequence 119, Application US/10125869A
; Publication No. US20030199671A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac Jesus
; APPLICANT: Wu, Qi-Long
; APPLICANT: Ley, Arthur C.
; APPLICANT: Stochl, Mark
; APPLICANT: Ransohoff, Thomas C.
; APPLICANT: Potter, M. Daniel (deceased)
; TITLE OF INVENTION: BINDING MOLECULES FOR Fc-REGION
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 3421.1006-001
; CURRENT APPLICATION NUMBER: US/10/125,869A
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/284,534
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 119
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc region binding polypeptide
US-10-125-869A-119

Query Match 41.9%; Score 26; DB 14; Length 15;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NFYKLP 9
||::||
Db 5 NFWQLP 10

RESULT 15

US-10-462-262-267

; Sequence 267, Application US/10462262
; Publication No. US20040009534A1
; GENERAL INFORMATION:

; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.
; TITLE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: 10280-052001
; CURRENT APPLICATION NUMBER: US/10/462,262
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 267
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin binding polypeptide
US-10-462-262-267

Query Match 41.9%; Score 26; DB 15; Length 15;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NFYKLP 9
||: ||
Db 5 NFWQLP 10

RESULT 16

US-10-462-262-343
; Sequence 343, Application US/10462262
; Publication No. US20040009534A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.
; TITLE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: 10280-052001
; CURRENT APPLICATION NUMBER: US/10/462,262
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 343
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin binding polypeptide
US-10-462-262-343

Query Match 41.9%; Score 26; DB 15; Length 15;
Best Local Similarity 66.7%; Pred. No. 7.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NFYKLP 9
||: ||
Db 5 NFWQLP 10

RESULT 17

US-09-799-576A-22

; Sequence 22, Application US/09799576A

; Patent No. US20020034774A1

; GENERAL INFORMATION:

; APPLICANT: HULTGREN, Scott

; KUEHN, Meta

; XU, Zheng

; OGG, Derek

; HARRIS, Mark

; LEPISTO, Matti

; KIHLEBERG, Jan

; JONES, Charles H.

; TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS

; FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL

INFECTIONS

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/799,576A

; FILING DATE: 07-Mar-2001

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/640,877

; FILING DATE: 10-OCT-1996

; APPLICATION NUMBER: WO PCT/US94/13455

; FILING DATE: 18-NOV-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Rea, Teresa Stanek

; REGISTRATION NUMBER: 30,427

; REFERENCE/DOCKET NUMBER: 016921-164

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 22:

US-09-799-576A-22

Query Match

41.9%; Score 26; DB 9; Length 16;

Best Local Similarity 57.1%; Pred. No. 7.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 QNFYKLP 9
|: ||:|
Db 9 QDHYKMP 15

RESULT 18

US-09-799-540-22

; Sequence 22, Application US/09799540

; Patent No. US20020045199A1

; GENERAL INFORMATION:

; APPLICANT: HULTGREN, Scott

; APPLICANT: KUEHN, Meta

; APPLICANT: XU, Zheng

; APPLICANT: OGG, Derek

; APPLICANT: HARRIS, Mark

; APPLICANT: LEPISTO, Matti

; APPLICANT: KIHLEBERG, Jan

; APPLICANT: JONES, Charles H.

; TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS

; TITLE OF INVENTION: FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL
INFECTIONS

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/799,540

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/640,877

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Rea, Teresa Stanek

; REGISTRATION NUMBER: 30,427

; REFERENCE/DOCKET NUMBER: 016921-122

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 22:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 16 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide
US-09-799-540-22

Query Match 41.9%; Score 26; DB 9; Length 16;
Best Local Similarity 57.1%; Pred. No. 7.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 QNFYKLP 9
|: ||:|
Db 9 QDHYKMP 15

RESULT 19

US-09-799-608-22

; Sequence 22, Application US/09799608

; Patent No. US20020146428A1

; GENERAL INFORMATION:

; APPLICANT: HULTGREN, Scott

; KUEHN, Meta

; XU, Zheng

; OGG, Derek

; HARRIS, Mark

; LEPISTO, Matti

; KIHLEBERG, Jan

; JONES, Charles H.

; TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS

; FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL
INFECTIONS

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/799,608

; FILING DATE: 07-Mar-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/640,877

; FILING DATE: <Unknown>

; APPLICATION NUMBER: WO PCT/US94/13455

; FILING DATE: 18-NOV-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Rea, Teresa Stanek

; REGISTRATION NUMBER: 30,427

; REFERENCE/DOCKET NUMBER: 016921-122

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-799-608-22

Query Match 41.9%; Score 26; DB 9; Length 16;
Best Local Similarity 57.1%; Pred. No. 7.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 QNFYKLP 9
|: ||:|
Db 9 QDHYKMP 15

RESULT 20
US-09-798-932-22
; Sequence 22, Application US/09798932
; Publication No. US20030198992A1
; GENERAL INFORMATION:
; APPLICANT: HULTGREN, Scott
; KUEHN, Meta
; XU, Zheng
; OGG, Derek
; HARRIS, Mark
; LEPISTO, Matti
; KIHLEBERG, Jan
; JONES, Charles H.
; TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS
; FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL
INFECTIONS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/798,932
; FILING DATE: 01-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/640,877
; FILING DATE: 10-OCT-1996
; APPLICATION NUMBER: WO PCT/US94/13455
; FILING DATE: 18-NOV-1994

; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa Stanek
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 016921-122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-798-932-22

Query Match 41.9%; Score 26; DB 10; Length 16;
Best Local Similarity 57.1%; Pred. No. 7.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 QNFYKLP 9
|: ||:|
Db 9 QDHYKMP 15

RESULT 21

US-09-799-680-22

; Sequence 22, Application US/09799680

; Publication No. US20030224468A1

; GENERAL INFORMATION:

; APPLICANT: HULTGREN, Scott

; APPLICANT: KUEHN, Meta

; APPLICANT: XU, Zheng

; APPLICANT: OGG, Derek

; APPLICANT: HARRIS, Mark

; APPLICANT: LEPISTO, Matti

; APPLICANT: KIHLEBERG, Jan

; APPLICANT: JONES, Charles H.

; TITLE OF INVENTION: COMPOUNDS AND PHARMACEUTICAL COMPOSITIONS

; TITLE OF INVENTION: FOR THE TREATMENT AND PROPHYLAXIS OF BACTERIAL

; TITLE OF INVENTION: INFECTIONS

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/799,680

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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/640,877
; FILING DATE: 10-OCT-1996
; APPLICATION NUMBER: WO PCT/US94/13455
; FILING DATE: 18-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Rea, Teresa Stanek
; REGISTRATION NUMBER: 30,427
; REFERENCE/DOCKET NUMBER: 016921-122
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-799-680-22

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Query Match          41.9%; Score 26; DB 12; Length 16;
Best Local Similarity 57.1%; Pred. No. 7.9e+02;
Matches      4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy      3 QNFYKLP 9
        |: ||:|
Db      9 QDHYKMP 15

```

```

RESULT 22
US-09-745-078A-21
; Sequence 21, Application US/09745078A
; Publication No. US20030050434A1
; GENERAL INFORMATION:
; APPLICANT: Garth J. S. COOPER
; APPLICANT: Christina M. BUCHANAN
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/09/745,078A
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: NZ336359
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-09-745-078A-21

```

Query Match 41.9%; Score 26; DB 10; Length 17;
Best Local Similarity 44.4%; Pred. No. 8.4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPQNFYKLP 9
:| || :|
Db 9 LPDNFPRYP 17

RESULT 23

US-09-962-756-1205

; Sequence 1205, Application US/09962756
; Publication No. US20030195147A1
; GENERAL INFORMATION:
; APPLICANT: PILLUTLA, RENUKA
; APPLICANT: BRISSETTE, RENEE
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: SCHAFFER, LAUGE
; APPLICANT: BRANDT, JAKOB
; APPLICANT: GOLDSTEIN, NEIL I.
; APPLICANT: SPETZLER, JANE
; APPLICANT: OSTERGAARD, SOREN
; APPLICANT: HANSEN, PER HERTZ
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4051US1
; CURRENT APPLICATION NUMBER: US/09/962,756
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1205
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-962-756-1205

Query Match 41.9%; Score 26; DB 10; Length 17;
Best Local Similarity 80.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PQNFY 6
| |||
Db 3 PSNFY 7

RESULT 24

US-09-962-756-1757

; Sequence 1757, Application US/09962756
; Publication No. US20030195147A1
; GENERAL INFORMATION:
; APPLICANT: PILLUTLA, RENUKA


```

; APPLICANT: BRISSETTE, RENEE
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: SCHAFFER, LAUGE
; APPLICANT: BRANDT, JAKOB
; APPLICANT: GOLDSTEIN, NEIL I.
; APPLICANT: SPETZLER, JANE
; APPLICANT: OSTERGAARD, SOREN
; APPLICANT: HANSEN, PER HERTZ
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4051US1
; CURRENT APPLICATION NUMBER: US/09/962,756
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1757
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-962-756-1757

```

```

Query Match          41.9%; Score 26; DB 10; Length 17;
Best Local Similarity 80.0%; Pred. No. 8.4e+02;
Matches      4; Conservative    0; Mismatches    1; Indels      0; Gaps      0;

```

```

QY      2 PQNFY 6
        | |||
Db      3 PSNFY 7

```

RESULT 25

```

US-09-962-756-1911
; Sequence 1911, Application US/09962756
; Publication No. US20030195147A1
; GENERAL INFORMATION:
; APPLICANT: PILLUTLA, RENUKA
; APPLICANT: BRISSETTE, RENEE
; APPLICANT: BLUME, ARTHUR J.
; APPLICANT: SCHAFFER, LAUGE
; APPLICANT: BRANDT, JAKOB
; APPLICANT: GOLDSTEIN, NEIL I.
; APPLICANT: SPETZLER, JANE
; APPLICANT: OSTERGAARD, SOREN
; APPLICANT: HANSEN, PER HERTZ
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4051US1
; CURRENT APPLICATION NUMBER: US/09/962,756
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127

```

; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1911
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-962-756-1911

Query Match 41.9%; Score 26; DB 10; Length 17;
Best Local Similarity 80.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PQNFY 6
| |||
Db 3 PSNFY 7

RESULT 26

US-10-374-624-21

; Sequence 21, Application US/10374624
; Publication No. US20030166561A1
; GENERAL INFORMATION:
; APPLICANT: Garth J. S. COOPER
; APPLICANT: Christina M. BUCHANAN
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/10/374,624
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US/09/745,078A
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: NZ336359
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-10-374-624-21

Query Match 41.9%; Score 26; DB 14; Length 17;
Best Local Similarity 44.4%; Pred. No. 8.4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPQNFYKLP 9
:| || :|
Db 9 LPDNFPRYP 17

RESULT 27

US-10-253-471-1205

; Sequence 1205, Application US/10253471
 ; Publication No. US20030236190A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PILLUTLA, RENUKA et al.
 ; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
 ; FILE REFERENCE: 1878-4057
 ; CURRENT APPLICATION NUMBER: US/10/253,471
 ; CURRENT FILING DATE: 2002-09-24
 ; PRIOR APPLICATION NUMBER: 09/962,756
 ; PRIOR FILING DATE: 2001-09-24
 ; PRIOR APPLICATION NUMBER: 09/538,038
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: 09/146,127
 ; PRIOR FILING DATE: 1998-09-02
 ; NUMBER OF SEQ ID NOS: 2227
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1205
 ; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: peptide

US-10-253-471-1205

Query Match 41.9%; Score 26; DB 15; Length 17;
 Best Local Similarity 80.0%; Pred. No. 8.4e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PQNFY 6
 | |||
 Db 3 PSNFY 7

RESULT 28

US-10-253-471-1757

; Sequence 1757, Application US/10253471
 ; Publication No. US20030236190A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PILLUTLA, RENUKA et al.
 ; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
 ; FILE REFERENCE: 1878-4057
 ; CURRENT APPLICATION NUMBER: US/10/253,471
 ; CURRENT FILING DATE: 2002-09-24
 ; PRIOR APPLICATION NUMBER: 09/962,756
 ; PRIOR FILING DATE: 2001-09-24
 ; PRIOR APPLICATION NUMBER: 09/538,038
 ; PRIOR FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: 09/146,127
 ; PRIOR FILING DATE: 1998-09-02
 ; NUMBER OF SEQ ID NOS: 2227
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1757
 ; LENGTH: 17
 ; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-253-471-1757

Query Match 41.9%; Score 26; DB 15; Length 17;
Best Local Similarity 80.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PQNFY 6
| |||
Db 3 PSNFY 7

RESULT 29

US-10-253-471-1911
; Sequence 1911, Application US/10253471
; Publication No. US20030236190A1
; GENERAL INFORMATION:
; APPLICANT: PILLUTLA, RENUKA et al.
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4057
; CURRENT APPLICATION NUMBER: US/10/253,471
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: 09/962,756
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1911
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-253-471-1911

Query Match 41.9%; Score 26; DB 15; Length 17;
Best Local Similarity 80.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PQNFY 6
| |||
Db 3 PSNFY 7

RESULT 30

US-10-253-493-1205
; Sequence 1205, Application US/10253493
; Publication No. US20040023887A1
; GENERAL INFORMATION:
; APPLICANT: PILLUTLA, RENUKA et al.

```
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4056
; CURRENT APPLICATION NUMBER: US/10/253,493
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: 09/962,756
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1205
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-253-493-1205
```

```
Query Match          41.9%; Score 26; DB 16; Length 17;
Best Local Similarity 80.0%; Pred. No. 8.4e+02;
Matches      4; Conservative      0; Mismatches      1; Indels      0; Gaps      0;
```

```
Qy      2 PQNFY 6
        | |||
Db      3 PSNFY 7
```

```
RESULT 31
US-10-253-493-1757
; Sequence 1757, Application US/10253493
; Publication No. US20040023887A1
; GENERAL INFORMATION:
; APPLICANT: PILLUTLA, RENUKA et al.
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4056
; CURRENT APPLICATION NUMBER: US/10/253,493
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: 09/962,756
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1757
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-253-493-1757
```

Query Match 41.9%; Score 26; DB 16; Length 17;
Best Local Similarity 80.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PQNFY 6
| |||
Db 3 PSNFY 7

RESULT 32

US-10-253-493-1911

; Sequence 1911, Application US/10253493
; Publication No. US20040023887A1
; GENERAL INFORMATION:
; APPLICANT: PILLUTLA, RENUKA et al.
; TITLE OF INVENTION: INSULIN AND IGF-1 RECEPTOR AGONISTS AND ANTAGONISTS
; FILE REFERENCE: 1878-4056
; CURRENT APPLICATION NUMBER: US/10/253,493
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: 09/962,756
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/538,038
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/146,127
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 2227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1911
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-253-493-1911

Query Match 41.9%; Score 26; DB 16; Length 17;
Best Local Similarity 80.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PQNFY 6
| |||
Db 3 PSNFY 7

RESULT 33

US-09-745-078A-20

; Sequence 20, Application US/09745078A
; Publication No. US20030050434A1
; GENERAL INFORMATION:
; APPLICANT: Garth J. S. COOPER
; APPLICANT: Christina M. BUCHANAN
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/09/745,078A
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: NZ336359

; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-09-745-078A-20

Query Match 41.9%; Score 26; DB 10; Length 18;
Best Local Similarity 44.4%; Pred. No. 9e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPQNFYKLP 9
 :| || : |
Db 9 LPDNFPRYP 17

RESULT 34

US-10-374-624-20
; Sequence 20, Application US/10374624
; Publication No. US20030166561A1
; GENERAL INFORMATION:
; APPLICANT: Garth J. S. COOPER
; APPLICANT: Christina M. BUCHANAN
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE: 441842000100
; CURRENT APPLICATION NUMBER: US/10/374,624
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US/09/745,078A
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: NZ336359
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/NZ00/00102
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of human preptin
US-10-374-624-20

Query Match 41.9%; Score 26; DB 14; Length 18;
Best Local Similarity 44.4%; Pred. No. 9e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPQNFYKLP 9
 :| || : |
Db 9 LPDNFPRYP 17

RESULT 35

US-09-756-283A-42

; Sequence 42, Application US/09756283A
 ; Patent No. US20020151478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chernajovsky, Yuti
 ; APPLICANT: Dreja, Hanna Stina
 ; APPLICANT: Adams, Gillian
 ; TITLE OF INVENTION: Latent Fusion Protein
 ; FILE REFERENCE: 0623.1000000
 ; CURRENT APPLICATION NUMBER: US/09/756,283A
 ; CURRENT FILING DATE: 2001-01-09
 ; NUMBER OF SEQ ID NOS: 100
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 42
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-756-283A-42

Query Match 40.3%; Score 25; DB 9; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.2e+06;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFY 6
 :|:|:
 Db 1 IPENFF 6

RESULT 36

US-09-756-283A-58

; Sequence 58, Application US/09756283A
 ; Patent No. US20020151478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chernajovsky, Yuti
 ; APPLICANT: Dreja, Hanna Stina
 ; APPLICANT: Adams, Gillian
 ; TITLE OF INVENTION: Latent Fusion Protein
 ; FILE REFERENCE: 0623.1000000
 ; CURRENT APPLICATION NUMBER: US/09/756,283A
 ; CURRENT FILING DATE: 2001-01-09
 ; NUMBER OF SEQ ID NOS: 100
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 58
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-756-283A-58

Query Match 40.3%; Score 25; DB 9; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.2e+06;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFY 6
 :|:|:
 Db 1 IPENFF 6

RESULT 37

US-09-756-283A-69

; Sequence 69, Application US/09756283A
 ; Patent No. US20020151478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chernajovsky, Yuti
 ; APPLICANT: Dreja, Hanna Stina
 ; APPLICANT: Adams, Gillian
 ; TITLE OF INVENTION: Latent Fusion Protein
 ; FILE REFERENCE: 0623.1000000
 ; CURRENT APPLICATION NUMBER: US/09/756,283A
 ; CURRENT FILING DATE: 2001-01-09
 ; NUMBER OF SEQ ID NOS: 100
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 69
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-756-283A-69

Query Match 40.3%; Score 25; DB 9; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.2e+06;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFY 6
 :|:|:
 Db 1 IPENFF 6

RESULT 38

US-09-756-283A-90

; Sequence 90, Application US/09756283A
 ; Patent No. US20020151478A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chernajovsky, Yuti
 ; APPLICANT: Dreja, Hanna Stina
 ; APPLICANT: Adams, Gillian
 ; TITLE OF INVENTION: Latent Fusion Protein
 ; FILE REFERENCE: 0623.1000000
 ; CURRENT APPLICATION NUMBER: US/09/756,283A
 ; CURRENT FILING DATE: 2001-01-09
 ; NUMBER OF SEQ ID NOS: 100
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 90
 ; LENGTH: 8
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-756-283A-90

Query Match 40.3%; Score 25; DB 9; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.2e+06;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFY 6
 :|:|:

Db 1 IPENFF 6

RESULT 39

US-09-756-283A-96

; Sequence 96, Application US/09756283A
; Patent No. US20020151478A1
; GENERAL INFORMATION:
; APPLICANT: Chernajovsky, Yuti
; APPLICANT: Dreja, Hanna Stina
; APPLICANT: Adams, Gillian
; TITLE OF INVENTION: Latent Fusion Protein
; FILE REFERENCE: 0623.1000000
; CURRENT APPLICATION NUMBER: US/09/756,283A
; CURRENT FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 96
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-756-283A-96

Query Match 40.3%; Score 25; DB 9; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNFY 6
:|:|:
Db 1 IPENFF 6

RESULT 40

US-10-078-968-2

; Sequence 2, Application US/10078968
; Publication No. US20020147148A1
; GENERAL INFORMATION:
; APPLICANT: Ensign, Jerald C
; APPLICANT: Bowen, David J
; APPLICANT: Tenor, Jennifer L
; APPLICANT: Ciche, Todd A
; APPLICANT: Petell, James K.
; APPLICANT: Strickland, James A
; APPLICANT: Orr, Gregory L
; APPLICANT: Fatig, Raymond
; APPLICANT: Bintrim, Scott
; TITLE OF INVENTION: INSECTICIDAL PROTEIN TOXINS FROM XENORHABDUS
; FILE REFERENCE: 50585A
; CURRENT APPLICATION NUMBER: US/10/078,968
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/072,264
; PRIOR FILING DATE: 1998-05-04
; PRIOR APPLICATION NUMBER: 60/045,641
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2

; LENGTH: 8
; TYPE: PRT
; ORGANISM: Xenorhabdus Wi
US-10-078-968-2

Query Match 40.3%; Score 25; DB 13; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 QNFYKLP 9
|| |: |
Db 2 QNVYRYP 8

RESULT 41

US-10-253-286-107

; Sequence 107, Application US/10253286
; Publication No. US20040058881A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: Ii-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2015
; CURRENT APPLICATION NUMBER: US/10/253,286
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Arachis hypogaea
US-10-253-286-107

Query Match 40.3%; Score 25; DB 12; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNF 5
:||||
Db 3 VPQNF 7

RESULT 42

US-10-245-871-107

; Sequence 107, Application US/10245871
; Publication No. US20030235594A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: Ii-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2013
; CURRENT APPLICATION NUMBER: US/10/245,871
; CURRENT FILING DATE: 2003-01-09

; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 107
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Arachis hypogaea
US-10-245-871-107

Query Match 40.3%; Score 25; DB 15; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNF 5
:||||
Db 3 VPQNF 7

RESULT 43

US-10-007-761-41
; Sequence 41, Application US/10007761
; Publication No. US20020150984A1
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; TITLE OF INVENTION: Peptides for Activation and Inhibition
; TITLE OF INVENTION: of delta-PKC
; FILE REFERENCE: 58600-8208.US00
; CURRENT APPLICATION NUMBER: US/10/007,761
; CURRENT FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/262,060
; PRIOR FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified delta V1-1 peptide
US-10-007-761-41

Query Match 40.3%; Score 25; DB 13; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.3e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 NFYKLPQM 11
| | : | | :
Db 3 NSYELPSL 10

RESULT 44

US-10-343-654-27
; Sequence 27, Application US/10343654
; Publication No. US20030204063A1

```
; GENERAL INFORMATION:
; APPLICANT: Denis Gravel (Inventor)
; APPLICANT: Abdelkrim Habi (Inventor)
; APPLICANT: Thierry Abribat (Inventor)
; APPLICANT: Theratechnologies Inc. (Assignee)
; TITLE OF INVENTION: Modified Biological Peptides with
; TITLE OF INVENTION: Increased Potency
; FILE REFERENCE: 12411-22PCT
; CURRENT APPLICATION NUMBER: US/10/343,654
; CURRENT FILING DATE: 2003-02-03
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: human
;   FEATURE:
;   NAME/KEY: AMIDATION
;   LOCATION: (11)...(11)
US-10-343-654-27
```

```
Query Match          40.3%; Score 25; DB 12; Length 11;
Best Local Similarity 50.0%; Pred. No. 8e+02;
Matches      4; Conservative      2; Mismatches      2; Indels      0; Gaps      0;
```

```
Qy      1 MPQNFYKL 8
        :|| |: |
Db      3 LPQEFFGL 10
```

```
RESULT 45
US-10-119-528-31
; Sequence 31, Application US/10119528
; Publication No. US20030175722A1
; GENERAL INFORMATION:
; APPLICANT: Mann, M.
; APPLICANT: Mortensen, P.
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR SEARCHING GENOMIC DATABASES
; FILE REFERENCE: MDSP-P01-004
; CURRENT APPLICATION NUMBER: US/10/119,528
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/282,551
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/285,362
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-10-119-528-31
```

```
Query Match          40.3%; Score 25; DB 14; Length 11;
Best Local Similarity 57.1%; Pred. No. 8e+02;
Matches      4; Conservative      1; Mismatches      2; Indels      0; Gaps      0;
```

Qy 5 FYKLPQM 11
|| || :
Db 1 FYSLPAL 7

RESULT 46

US-09-813-653-27

; Sequence 27, Application US/09813653
; Patent No. US20020064770A1
; GENERAL INFORMATION:
; APPLICANT: Nestor, John
; APPLICANT: Wilson, Carol
; APPLICANT: See, Raymond
; APPLICANT: Tan Hehir, Christina
; TITLE OF INVENTION: Binding Compounds and Methods For Identifying Binding Compounds
; FILE REFERENCE: CNS-005
; CURRENT APPLICATION NUMBER: US/09/813,653
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,946
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/190,996
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/191,299
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence identified through phage display for CCR5 binding
US-09-813-653-27

Query Match 40.3%; Score 25; DB 9; Length 12;
Best Local Similarity 40.0%; Pred. No. 8.8e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PQNFYKLPQM 11
| :|| | :
Db 2 PADFYSHPAL 11

RESULT 47

US-09-865-018-10

; Sequence 10, Application US/09865018
; Patent No. US20020110886A1
; GENERAL INFORMATION:
; APPLICANT: Massague, Joan
; Roberts, James M.
; Koff, Andrew
; Polyak, Kornelia
; TITLE OF INVENTION: ISOLATED p27 PROTEIN AND METHOD FOR ITS PRODUCTION AND USE
; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 ; STREET: One Post Office Square
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02109-2170
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/865,018
 ; FILING DATE: 24-May-2001
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/854,039
 ; FILING DATE: 09-MAY-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Vincent, Matthew P.
 ; REGISTRATION NUMBER: 36,709
 ; REFERENCE/DOCKET NUMBER: MIV-079.04
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617-832-1000
 ; TELEFAX: 617-832-7000
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 12 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 US-09-865-018-10

Query Match 40.3%; Score 25; DB 9; Length 12;
 Best Local Similarity 30.0%; Pred. No. 8.8e+02;
 Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPQNFYKLPQ 10
 :|: :|: |:
 Db 1 LPEFYRPPR 10

RESULT 48

US-09-845-612B-10
 ; Sequence 10, Application US/09845612B
 ; Publication No. US20030083261A1
 ; GENERAL INFORMATION:
 ; APPLICANT: YU, HONGTAO
 ; APPLICANT: TANG, ZHANYUN
 ; APPLICANT: LUO, XUELIAN
 ; APPLICANT: RIZO-REY, JOSE
 ; TITLE OF INVENTION: A CLASS OF 12MER PEPTIDES THAT INHIBIT THE FUNCTION OF
 THE MITOTIC CHECK
 ; TITLE OF INVENTION: POINT PROTEIN MAD2
 ; FILE REFERENCE: UTSD:795

; CURRENT APPLICATION NUMBER: US/09/845,612B
; CURRENT FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(12)
; OTHER INFORMATION: synthetic peptide
US-09-845-612B-10

Query Match 40.3%; Score 25; DB 10; Length 12;
Best Local Similarity 66.7%; Pred. No. 8.8e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYKLPQ 10
:||||:
Db 2 WYKLPK 7

RESULT 49

US-10-253-286-120

; Sequence 120, Application US/10253286
; Publication No. US20040058881A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: Ii-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2015
; CURRENT APPLICATION NUMBER: US/10/253,286
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 120
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Ii-key/Ara h 3 hybrid peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)
; OTHER INFORMATION: a-aminovaleric acid
; FEATURE:
; OTHER INFORMATION: C-term amidated
US-10-253-286-120

Query Match 40.3%; Score 25; DB 12; Length 14;
Best Local Similarity 80.0%; Pred. No. 1e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNF 5
:||||
Db 8 VPQNF 12

RESULT 50

US-10-245-871-120

; Sequence 120, Application US/10245871

; Publication No. US20030235594A1

; GENERAL INFORMATION:

; APPLICANT: HUMPHREYS, ROBERT

; APPLICANT: XU, MINZHEN

; TITLE OF INVENTION: Ii-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES

; FILE REFERENCE: REH-2013

; CURRENT APPLICATION NUMBER: US/10/245,871

; CURRENT FILING DATE: 2003-01-09

; PRIOR APPLICATION NUMBER: 10/197,000

; PRIOR FILING DATE: 2002-07-17

; PRIOR APPLICATION NUMBER: 09/396,813

; PRIOR FILING DATE: 1999-09-14

; NUMBER OF SEQ ID NOS: 905

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 120

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Ii-key/Ara h 3 hybrid peptide

; FEATURE:

; NAME/KEY: MOD_RES

; LOCATION: (5)

; OTHER INFORMATION: a-aminovaleric acid

; FEATURE:

; OTHER INFORMATION: C-term amidated

US-10-245-871-120

Query Match 40.3%; Score 25; DB 15; Length 14;

Best Local Similarity 80.0%; Pred. No. 1e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQNF 5
:||||
Db 8 VPQNF 12

Search completed: July 4, 2004, 05:12:29

Job time : 23.5896 secs

OM protein - protein search, using sw model

```
Run on:      July  4, 2004, 04:33:51 ; Search time 18.7164 Seconds
              (without alignments)
              185.436 Million cell updates/sec
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Title: US-09-641-802-6
Perfect score: 62
Sequence: 1 MPQNFYKLPQM 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 5664

```
Minimum DB seq length: 7
Maximum DB seq length: 18
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 100 summaries
```

```
Database :
SPREMBL_25:*
1:  sp_archea:*
2:  sp_bacteria:*
3:  sp_fungi:*
4:  sp_human:*
5:  sp_invertebrate:*
6:  sp_mammal:*
7:  sp_mhc:*
8:  sp_organelle:*
9:  sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID		Description

1	25	40.3	17	10	O49225	O49225 glycine max
2	25	40.3	17	10	Q41400	Q41400 sesbania ro
3	22	35.5	14	8	Q9MJQ3	Q9mjQ3 podospo
4	22	35.5	15	1	Q9UWM1	Q9uwm1 methanospir
5	22	35.5	15	2	P82999	P82999 pseudomonas
6	22	35.5	17	4	Q9UCA4	Q9uca4 homo sapien
7	21	33.9	10	2	Q9XBH3	Q9xbh3 bacillus ce
8	21	33.9	13	11	Q9QVL4	Q9qvl4 rattus sp.
9	21	33.9	15	6	Q9TQX7	Q9tqx7 bos taurus
10	21	33.9	18	2	Q9RGR2	Q9rgr2 bordetella
11	21	33.9	18	2	Q9RGR1	Q9rgr1 bordetella
12	20	32.3	11	2	Q9RFZ2	Q9rfz2 mycoplasma
13	20	32.3	11	4	Q16234	Q16234 homo sapien
14	20	32.3	12	2	Q53579	Q53579 rhodobacter
15	20	32.3	13	8	Q9THR8	Q9thr8 bryopsis sp
16	20	32.3	13	8	Q9TKG6	Q9tkg6 lambia anta
17	20	32.3	13	13	Q8JJ32	Q8jj32 ficedula al
18	20	32.3	15	2	Q53580	Q53580 rhodobacter
19	20	32.3	15	2	Q9R4T2	Q9r4t2 bacillus in
20	20	32.3	15	6	Q9TR40	Q9tr40 bos taurus
21	20	32.3	15	6	Q9TQQ9	Q9tqq9 bos taurus
22	20	32.3	17	11	Q9QUY6	Q9quy6 rattus sp.
23	20	32.3	18	8	Q8SKY0	Q8sky0 cuscute ref
24	19	30.6	8	2	Q45615	Q45615 bacillus su
25	19	30.6	8	4	Q9HCQ0	Q9hcg0 homo sapien
26	19	30.6	9	12	Q67605	Q67605 squash leaf
27	19	30.6	9	12	Q67606	Q67606 squash leaf
28	19	30.6	11	3	Q9URG1	Q9urg1 neurospora
29	19	30.6	11	12	Q80GN9	Q80gn9 tomato leaf
30	19	30.6	13	8	Q9T4K5	Q9t4k5 bryopsis sp
31	19	30.6	13	8	Q9THS3	Q9ths3 bryopsis sp
32	19	30.6	13	8	Q9T4K4	Q9t4k4 bryopsis sp
33	19	30.6	13	8	Q9THS2	Q9ths2 bryopsis sp
34	19	30.6	13	8	Q9T4K6	Q9t4k6 bryopsis sp
35	19	30.6	13	8	Q9T4K3	Q9t4k3 bryopsis sp
36	19	30.6	16	8	Q34699	Q34699 helianthus
37	19	30.6	16	9	Q38671	Q38671 bacterioph
38	19	30.6	17	4	Q13376	Q13376 homo sapien
39	19	30.6	17	6	Q9XSG1	Q9xsg1 bos taurus
40	19	30.6	17	13	Q9PRU8	Q9pru8 gallus gall
41	19	30.6	18	2	Q9ZG42	Q9zg42 chlamydia t
42	19	30.6	18	6	O97773	O97773 cercopithe
43	19	30.6	18	6	Q7YRH7	Q7yrh7 sus scrofa
44	19	30.6	18	11	Q7TNW8	Q7tnw8 rattus norv
45	19	30.6	18	11	Q7TNW7	Q7tnw7 mus musculu
46	18	29.0	8	11	Q62527	Q62527 mus spretus
47	18	29.0	9	8	Q94VG2	Q94vg2 varanus ind
48	18	29.0	9	10	Q9S8J8	Q9s8j8 oryza sativ
49	18	29.0	10	4	Q9H121	Q9h121 homo sapien
50	18	29.0	13	4	Q14462	Q14462 homo sapien
51	18	29.0	13	8	Q9MQK0	Q9mqk0 cervus elap
52	18	29.0	14	2	Q45876	Q45876 clostridium
53	18	29.0	14	2	Q45872	Q45872 clostridium
54	18	29.0	14	8	Q8HR43	Q8hr43 clivia mini
55	18	29.0	14	12	Q84072	Q84072 influenzavi
56	18	29.0	14	13	Q91777	Q91777 xenopus lae
57	18	29.0	15	2	Q9X637	Q9x637 klebsiella

58	18	29.0	15	2	Q9X635	Q9x635 escherichia
59	18	29.0	15	3	Q9URC5	Q9urc5 saccharomyc
60	18	29.0	15	4	Q9UC83	Q9uc83 homo sapien
61	18	29.0	15	5	P81831	P81831 chlamydomon
62	18	29.0	15	10	P82331	P82331 pisum sativ
63	18	29.0	17	4	Q16231	Q16231 homo sapien
64	18	29.0	17	8	Q07055	Q07055 crithidia f
65	18	29.0	18	2	Q9R4C6	Q9r4c6 agrobacteri
66	18	29.0	18	4	Q8NED1	Q8ned1 homo sapien
67	18	29.0	18	10	Q8LNN9	Q8lnn9 oryza sativ
68	18	29.0	18	13	Q9PRR7	Q9prrr7 gallus gall
69	17	27.4	8	2	Q7X139	Q7x139 staphylococ
70	17	27.4	8	11	Q99P40	Q99p40 mus musculu
71	17	27.4	9	4	Q14715	Q14715 homo sapien
72	17	27.4	9	4	Q9UK44	Q9uk44 homo sapien
73	17	27.4	9	8	P92072	P92072 euhadra her
74	17	27.4	10	2	O54217	O54217 staphylococ
75	17	27.4	10	2	Q93UU2	Q93uu2 escherichia
76	17	27.4	10	8	Q9MJQ5	Q9mjq5 podospora c
77	17	27.4	10	13	Q7ZZI2	Q7zzi2 salvelinus
78	17	27.4	12	2	Q8KH47	Q8kh47 enterococcu
79	17	27.4	13	2	Q8KY46	Q8ky46 enterococcu
80	17	27.4	14	2	Q9R2Z4	Q9r2z4 campylobact
81	17	27.4	14	2	Q9R2Z5	Q9r2z5 campylobact
82	17	27.4	14	2	Q9X715	Q9x715 campylobact
83	17	27.4	14	2	Q9WW79	Q9ww79 campylobact
84	17	27.4	15	2	P83076	P83076 bacillus ce
85	17	27.4	15	6	Q9TR03	Q9tr03 bos taurus
86	17	27.4	15	7	Q9TNQ1	Q9tnq1 mus sp. bet
87	17	27.4	16	2	Q8KMS4	Q8kms4 escherichia
88	17	27.4	16	2	Q55090	Q55090 shigella so
89	17	27.4	16	4	Q9UMJ9	Q9umj9 homo sapien
90	17	27.4	16	6	Q28324	Q28324 capra hircu
91	17	27.4	16	6	Q9TRJ5	Q9trj5 bos taurus
92	17	27.4	16	10	P83635	P83635 oryza sativ
93	17	27.4	16	12	Q99154	Q99154 sendai viru
94	17	27.4	17	4	Q92727	Q92727 homo sapien
95	17	27.4	17	6	O46473	O46473 felis silve
96	17	27.4	17	6	Q95KQ7	Q95kq7 sus scrofa
97	17	27.4	17	6	Q95JA1	Q95jal sus scrofa
98	17	27.4	17	11	Q9QVM8	Q9qvm8 rattus sp.
99	17	27.4	18	2	Q47137	Q47137 escherichia
100	17	27.4	18	2	Q8VNJ9	Q8vnj9 haemophilus

ALIGNMENTS

RESULT 1

O49225

ID O49225 PRELIMINARY; PRT; 17 AA.

AC O49225;

DT 01-JUN-1998 (TrEMBLrel. 06, Created)

DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Hydroxyproline-rich glycoprotein (Fragment).

GN HRGP.

OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Essex; TISSUE=Root;
 RX MEDLINE=94211912; PubMed=8159793;
 RA Hong J.C., Cheong Y.H., Nagao R.T., Bahk J.D., Cho M.J., Key J.L.;
 RT "Isolation and characterization of three soybean extensin cDNAs."
 RL Plant Physiol. 104:793-796(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Essex; TISSUE=Root;
 RA Mahalingam R., Knap H.T.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF047052; AAC03558.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 17 AA; 2149 MW; 285E5874515A2222 CRC64;

Query Match 40.3%; Score 25; DB 10; Length 17;
 Best Local Similarity 50.0%; Pred. No. 8e+02;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PQNFYKLP 9
 | :|||
 Db 4 PHYYYYKSP 11

RESULT 2

Q41400

ID Q41400 PRELIMINARY; PRT; 17 AA.
 AC Q41400;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hydroxyproline-rich protein (Fragment).
 OS Sesbania rostrata.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Robinieae; Sesbania.
 OX NCBI_TaxID=3895;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sesbania rostrata;
 RC TISSUE=Bacterial infected stem located root primordia;
 RX MEDLINE=96112737; PubMed=8664492;
 RA Goormachtig S., Valerio-Lepiniec M., Szczyglowski K., Van Montagu M.,
 RA Holsters M., De Bruijn F.;
 RT "Use of differential display to identify novel Sesbania rostrata genes
 RT enhanced by Azorhizobium caulinodans infection."
 RL Mol. Plant Microbe Interact. 8:816-824(1995).
 DR EMBL; Z48673; CAA88592.1; -.
 DR PIR; S57991; S57991.
 FT NON_TER 1 1
 SQ SEQUENCE 17 AA; 2078 MW; 5060D27444515A22 CRC64;

Query Match 40.3%; Score 25; DB 10; Length 17;
Best Local Similarity 50.0%; Pred. No. 8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PQNFYKLP 9
| :|||
Db 3 PHYYYKSP 10

RESULT 3

Q9MJQ3

ID Q9MJQ3 PRELIMINARY; PRT; 14 AA.
AC Q9MJQ3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome b (Fragment).
GN CYTB.
OS Podospora curvicolla.
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora.
OX NCBI_TaxID=48157;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V;
RX MEDLINE=20150243; PubMed=10684923;
RA Saguez C., Lecellier G., Koll F.;
RT "Intronic GIY-YIG endonuclease gene in the mitochondrial genome of
RT Podospora curvicolla: evidence for mobility."
RL Nucleic Acids Res. 28:1299-1306(2000).
DR EMBL; AJ249985; CAB72449.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR005798; Cytb_b6_C.
DR PROSITE; PS00193; CYTOCHROME_B_QO; 1.
KW Mitochondrion.
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1603 MW; 2972D7731A723E43 CRC64;

Query Match 35.5%; Score 22; DB 8; Length 14;
Best Local Similarity 57.1%; Pred. No. 2.4e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 FYKLPQM 11
:| |||
Db 7 WYLLPSM 13

RESULT 4

Q9UWM1

ID Q9UWM1 PRELIMINARY; PRT; 15 AA.
AC Q9UWM1;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Benzoyl-CoA ligase (Fragment).
 OS Methanospirillum hungatei.
 OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
 OC Methanomicrobiales; Methanospirillaceae; Methanospirillum.
 OX NCBI_TaxID=2203;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93040109; PubMed=1369492;
 RA Auburger G., Winter J.;
 RL Appl. Microbiol. Biotechnol. 37:789-795(1992).
 DR PIR; A48372; A48372.
 SQ SEQUENCE 15 AA; 1880 MW; D2972EF3E690AC5C CRC64;

Query Match 35.5%; Score 22; DB 1; Length 15;
 Best Local Similarity 60.0%; Pred. No. 2.6e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PQNFY 6
 | : | |
 Db 5 PEEFY 9

RESULT 5
 P82999

ID P82999 PRELIMINARY; PRT; 15 AA.
 AC P82999;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Glutathione S-transferase (EC 2.5.1.18) (Fragment).
 OS Pseudomonas sp. (strain M1).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=95619;
 RN [1]
 RP SEQUENCE, FUNCTION, CATALYTIC ACTIVITY, SUBUNIT, AND SUBCELLULAR
 RP LOCATION.
 RX PubMed=11900268;
 RA Santos P.M., Mignogna G., Heipieper H.J., Zennaro E.;
 RT "Occurrence and properties of glutathione S-transferases in phenol-
 RT degrading Pseudomonas strains."
 RL Res. Microbiol. 153:89-98(2002).
 CC -!- FUNCTION: CONJUGATION OF REDUCED GLUTATHIONE TO A WIDE NUMBER OF
 CC EXOGENOUS AND ENDOGENOUS HYDROPHOBIC ELECTROPHILES.
 CC -!- CATALYTIC ACTIVITY: RX + GLUTATHIONE = HX + R-S-GLUTATHIONE.
 CC -!- SUBUNIT: MONOMER AND HOMODIMER.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE GST SUPERFAMILY.
 DR GO; GO:0005737; C:cytoplasm; NAS.
 DR GO; GO:0004364; F:glutathione transferase activity; NAS.
 DR GO; GO:0006803; P:glutathione conjugation reaction; NAS.
 KW Transferase.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1817 MW; 0E2A0FC5F55CBAC2 CRC64;

Query Match 35.5%; Score 22; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 FYKLPQ 10
|| ||
Db 7 FYHSPQ 12

RESULT 6

Q9UCA4

ID Q9UCA4 PRELIMINARY; PRT; 17 AA.
AC Q9UCA4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Tumor necrosis factor inhibitor I (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=94286045; PubMed=8015639;
RA Suzuki J., Tomizawa S., Arai H., Seki Y., Maruyama K., Kuroume T.;
RT "Purification of two types of TNF inhibitors in the urine of the
RT patient with chronic glomerulonephritis."
RL Nephron 66:386-390(1994).
SQ SEQUENCE 17 AA; 1903 MW; D4418485E6981B28 CRC64;

Query Match 35.5%; Score 22; DB 4; Length 17;
Best Local Similarity 55.6%; Pred. No. 2.9e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PQNFYKLPQ 10
|| | ||
Db 5 PQGKYIHPQ 13

RESULT 7

Q9XBH3

ID Q9XBH3 PRELIMINARY; PRT; 10 AA.
AC Q9XBH3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Celf-like protein (Fragment).
GN CELF.
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10987;
RX MEDLINE=99231848; PubMed=10217496;
RA Okstad O.A., Hegna I., Lindbaeck T., Rishovd A.L., Kolsto A.B.;

RT "Genome organisation is not conserved between Bacillus cereus and
RT Bacillus subtilis.";
RL Microbiology 145:621-631(1999).
DR EMBL; AJ000394; CAB40625.1; -.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1264 MW; D3757EC33339C9D6 CRC64;

Query Match 33.9%; Score 21; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MPQNFYKL 8
:| | | |:
Db 1 LPQFFKKV 8

RESULT 8

Q9QVL4

ID Q9QVL4 PRELIMINARY; PRT; 13 AA.
AC Q9QVL4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 90 kDa advanced glycosylation ENDPRODUCT binding protein
DE (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=91341412; PubMed=1651976;
RA Yang Z., Makita Z., Horii Y., Brunelle S., Cerami A., Sehajpal P.,
RA Suthanthiran M., Vlassara H.;
RT "Two novel rat liver membrane proteins that bind advanced
RT glycosylation endproducts: relationship to macrophage receptor for
RT glucose-modified proteins.";
RL J. Exp. Med. 174:515-524(1991).
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1466 MW; 349E02EEFCFE9AB7 CRC64;

Query Match 33.9%; Score 21; DB 11; Length 13;
Best Local Similarity 80.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 KLPQM 11
| | | |
Db 4 KLPDM 8

RESULT 9

Q9TQX7

ID Q9TQX7 PRELIMINARY; PRT; 15 AA.
AC Q9TQX7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Cartilage oligomeric matrix protein (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95046341; PubMed=7957930;
 RA DiCesare P., Hauser N., Lehman D., Pasumarti S., Paulsson M.;
 RT "Cartilage oligomeric matrix protein (COMP) is an abundant component
 RT of tendon.";
 RL FEBS Lett. 354:237-240(1994).
 SQ SEQUENCE 15 AA; 1689 MW; D709168394B5861C CRC64;

Query Match 33.9%; Score 21; DB 6; Length 15;
 Best Local Similarity 42.9%; Pred. No. 4e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 FYKLPQM 11
 ||: |::
 Db 1 FYEGPEL 7

RESULT 10

Q9RGR2

ID Q9RGR2 PRELIMINARY; PRT; 18 AA.
 AC Q9RGR2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Adhesin (Fragment).
 GN FHAB.
 OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Alcaligenaceae; Bordetella.
 OX NCBI_TaxID=518;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RB50;
 RX MEDLINE=20290246; PubMed=10832649;
 RA Jacob-Dubuisson F., Kehoe B., Willery E., Reveneau N., Loch C.,
 RA Relman D.A.;
 RT "Molecular characterization of Bordetella bronchiseptica filamentous
 RT hemagglutinin and its secretion machinery.";
 RL Microbiology 146:1211-1221(2000).
 DR EMBL; AF111797; AAF21947.1; -.
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2151 MW; F139E793B031E143 CRC64;

Query Match 33.9%; Score 21; DB 2; Length 18;
 Best Local Similarity 50.0%; Pred. No. 4.8e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPQNFYKL 8
 | | |::|

Db 1 MNTNLYRL 8

RESULT 11

Q9RGR1

ID Q9RGR1 PRELIMINARY; PRT; 18 AA.
AC Q9RGR1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Adhesin (Fragment).
GN FHAB.
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=8234;
RX MEDLINE=20290246; PubMed=10832649;
RA Jacob-Dubuisson F., Kehoe B., Willery E., Reveneau N., Loch C.,
RA Relman D.A.;
RT "Molecular characterization of Bordetella bronchiseptica filamentous
RT hemagglutinin and its secretion machinery."
RL Microbiology 146:1211-1221(2000).
DR EMBL; AF111798; AAF21948.1; -.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2135 MW; F129A793B031E143 CRC64;

Query Match 33.9%; Score 21; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 4.8e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPQNFYKL 8
| | | : |
Db 1 MNTNLYRL 8

RESULT 12

Q9RFZ2

ID Q9RFZ2 PRELIMINARY; PRT; 11 AA.
AC Q9RFZ2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fructose biphosphate aldolase (Fragment).
GN FBA.
OS Mycoplasma mycoides subsp. capri.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=40477;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PG3;
RX MEDLINE=20193983; PubMed=10727835;
RA Thiaucourt F., Lorenzon S., David A., Breard A.;
RT "Phylogeny of the Mycoplasma mycoides cluster as shown by sequencing
RT of a putative membrane protein gene.";

RL Vet. Microbiol. 72:251-268(2000).
DR EMBL; AF162998; AAF15255.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1371 MW; 50B0881A3331FB57 CRC64;

Query Match 32.3%; Score 20; DB 2; Length 11;
Best Local Similarity 42.9%; Pred. No. 4.5e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPQNFYK 7
||: ::|
Db 1 MPKLYHK 7

RESULT 13

Q16234

ID Q16234 PRELIMINARY; PRT; 11 AA.
AC Q16234;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE HuD protein (Fragment).
GN HUD.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94349312; PubMed=8069866;
RA Sekido Y., Bader S.A., Carbone D.P., Johnson B.E., Minna J.D.;
RT "Molecular analysis of the HuD gene encoding a paraneoplastic
RT encephalomyelitis antigen in human lung cancer cell lines.";
RL Cancer Res. 54:4988-4992(1994).
DR EMBL; S73887; AAD14142.1; -.
DR PIR; I52708; I52708.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1289 MW; 2EDCF20E204415A7 CRC64;

Query Match 32.3%; Score 20; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 4.5e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPQNFYKL 8
|| ||
Db 3 MPSRILKL 10

RESULT 14

Q53579

ID Q53579 PRELIMINARY; PRT; 12 AA.
AC Q53579;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Light-harvesting complex I alpha polypeptide (Fragment).
GN PUFA.

OS Rhodobacter capsulatus (Rhodopseudomonas capsulata).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
 OC Rhodobacteraceae; Rhodobacter.
 OX NCBI_TaxID=1061;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92234963; PubMed=1569029;
 RA Richter P., Brand M., Drews G.;
 RT "Characterization of LHI- and LHI+ Rhodobacter capsulatus pufA
 RT mutants.";
 RL J. Bacteriol. 174:3030-3041(1992).
 DR EMBL; S97551; AAC60405.1; -.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1627 MW; 0F92F6EA8A70532B CRC64;

Query Match 32.3%; Score 20; DB 2; Length 12;
 Best Local Similarity 75.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYKL 8
 |||:
 Db 4 FYKI 7

RESULT 15

Q9THR8

ID Q9THR8 PRELIMINARY; PRT; 13 AA.
 AC Q9THR8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE PbsH (Fragment).
 GN PBSH.
 OS Bryopsis sp. A.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpales;
 OC Bryopsidaceae; Bryopsis.
 OX NCBI_TaxID=103784;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=98-02-01;
 RA Krellwitz E.C., Kowallik K.V., Manos P.S.;
 RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
 RT Atlantic and Caribbean based on Coding and Non-coding sequences of the
 RT Chloroplast psbB Operon.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF170413; AAD56858.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1785 MW; 3F9A1C3E247D0323 CRC64;

Query Match 32.3%; Score 20; DB 8; Length 13;
 Best Local Similarity 42.9%; Pred. No. 5.3e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MPQNFYK 7

|| :|
Db 1 MPXXYWK 7

RESULT 16

Q9TKG6

ID Q9TKG6 PRELIMINARY; PRT; 13 AA.
AC Q9TKG6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PbsH (Fragment).
GN PBSH.
OS *Lambia antarctica*.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpaceae;
OC Bryopsidaceae; *Lambia*.
OX NCBI_TaxID=101717;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lambia;
RA Krellwitz E.C., Kowallik K.V., Manos P.S.;
RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
RT Atlantic and Caribbean based on Coding and Non-coding sequences of the
RT Chloroplast psbB Operon."
RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF170416; AAD56864.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1423 MW; 8331687A3B73A321 CRC64;

Query Match 32.3%; Score 20; DB 8; Length 13;
Best Local Similarity 57.1%; Pred. No. 5.3e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MPQNFYK 7
||:| |
Db 1 MPKNSTK 7

RESULT 17

Q8JJ32

ID Q8JJ32 PRELIMINARY; PRT; 13 AA.
AC Q8JJ32;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE 37LRP/p40 (Fragment).
OS *Ficedula albicollis*.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; *Ficedula*.
OX NCBI_TaxID=59894;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B8;
RX MEDLINE=21918460; PubMed=11918793;

RA Primmer C.R., Borge T., Lindell J., Saetre G.-P.;
RT "Single-nucleotide polymorphism characterization in species with
RT limited available sequence information: high nucleotide diversity
RT revealed in the avian genome.";
RL Mol. Ecol. 11:603-612(2002).
DR EMBL; AF454232; AAM22911.1; -.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1674 MW; 18331625CF9559DB CRC64;

Query Match 32.3%; Score 20; DB 13; Length 13;
Best Local Similarity 50.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 FYKLPQ 10
||: |:
Db 7 FYRDPE 12

RESULT 18

Q53580

ID Q53580 PRELIMINARY; PRT; 15 AA.
AC Q53580;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Light-harvesting complex I alpha polypeptide (Fragment).
GN PUFA.
OS Rhodobacter capsulatus (Rhodopseudomonas capsulata).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;
OC Rhodobacteraceae; Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92234963; PubMed=1569029;
RA Richter P., Brand M., Drews G.;
RT "Characterization of LHI- and LHI+ Rhodobacter capsulatus pufA
RT mutants.";
RL J. Bacteriol. 174:3030-3041(1992).
DR EMBL; S97552; AAC60406.1; -.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 2054 MW; 3561FE413591D31A CRC64;

Query Match 32.3%; Score 20; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYKL 8
|||:
Db 4 FYKI 7

RESULT 19

Q9R4T2

ID Q9R4T2 PRELIMINARY; PRT; 15 AA.
AC Q9R4T2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Serine proteinase (Fragment).
 OS Bacillus intermedius.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1400;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95119214; PubMed=7819414;
 RA Balaban N.P., Sharipova M.R., Itskovich E.L., Leshchinskaia I.B.,
 RA Rudenskaia G.N.;
 RT "[Secreted serine proteinase from the spore-forming bacteria Bacillus
 RT intermedius 3-19].";
 RL Biokhimiia 59:1393-1400(1994).
 SQ SEQUENCE 15 AA; 1554 MW; 17125581FE06C265 CRC64;

Query Match 32.3%; Score 20; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 6.2e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 YKLPQM 11
 | :||:
 Db 6 YGIPQI 11

RESULT 20

Q9TR40

ID Q9TR40 PRELIMINARY; PRT; 15 AA.
 AC Q9TR40;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Glutamate dehydrogenase isoform II (EC 1.4.1.2) (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96061967; PubMed=7588764;
 RA Cho S.W., Lee J., Choi S.Y.;
 RT "Two soluble forms of glutamate dehydrogenase isoproteins from bovine
 RT brain.";
 RL Eur. J. Biochem. 233:340-346(1995).
 DR GO; GO:0004352; F:glutamate dehydrogenase activity; IEA.
 SQ SEQUENCE 15 AA; 1724 MW; 65F7CD91023AF925 CRC64;

Query Match 32.3%; Score 20; DB 6; Length 15;
 Best Local Similarity 75.0%; Pred. No. 6.2e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NFYK 7
 ||:|
 Db 12 NFFK 15

RESULT 21

Q9TQQ9

ID Q9TQQ9 PRELIMINARY; PRT; 15 AA.
AC Q9TQQ9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Glutamate dehydrogenase isoform I (EC 1.4.1.2) (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=96061967; PubMed=7588764;
RA Cho S.W., Lee J., Choi S.Y.;
RT "Two soluble forms of glutamate dehydrogenase isoproteins from bovine
RT brain.";
RL Eur. J. Biochem. 233:340-346(1995).
RN [2]
RP SEQUENCE.
RX MEDLINE=96043916; PubMed=7581004;
RA Lee J., Kim S.W., Cho S.W.;
RT "A novel glutamate dehydrogenase from bovine brain: purification and
RT characterization.";
RL Biochem. Mol. Biol. Int. 36:1087-1096(1995).
DR GO; GO:0004352; F:glutamate dehydrogenase activity; IEA.
SQ SEQUENCE 15 AA; 1754 MW; 65F7CD91023AEEBA CRC64;

Query Match 32.3%; Score 20; DB 6; Length 15;
Best Local Similarity 75.0%; Pred. No. 6.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NFYK 7
||:|
Db 12 NFFK 15

RESULT 22

Q9QUY6

ID Q9QUY6 PRELIMINARY; PRT; 17 AA.
AC Q9QUY6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Oligodendrocyte-specific UDP-galactose:ceramide galactosyltransferase
DE (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=96085162; PubMed=8521863;
RA Schulte S., Stoffel W.;
RT "UDP galactose:ceramide galactosyltransferase and glutamate/aspartate

RT transporter. Copurification, separation and characterization of the two
RT glycoproteins.";
RL Eur. J. Biochem. 233:947-953(1995).
SQ SEQUENCE 17 AA; 2017 MW; 0F92A645FFD7F828 CRC64;

Query Match 32.3%; Score 20; DB 11; Length 17;
Best Local Similarity 75.0%; Pred. No. 7e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQN 4
:|||
Db 5 LPQN 8

RESULT 23

Q8SKY0

ID Q8SKY0 PRELIMINARY; PRT; 18 AA.
AC Q8SKY0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein S11 (Fragment).
GN RPS11.
OS Cuscuta reflexa (Southern Asian dodder).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiids; Solanales; Convolvulaceae; Cuscuta.
OX NCBI_TaxID=4129;
RN [1]
RP SEQUENCE FROM N.A.
RA Berg S.;
RT "Sequence analysis and coding potential of the holoparasitic flowering
RT plant genus Cuscuta.";
RL Thesis (2002), Department of Institute of Botany,..
DR EMBL; AJ439611; CAD28796.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR001971; Ribosomal_S11.
DR Pfam; PF00411; Ribosomal_S11; 1.
KW Chloroplast.
FT NON_TER 1 1
SQ SEQUENCE 18 AA; 2088 MW; 130D427BFE680B24 CRC64;

Query Match 32.3%; Score 20; DB 8; Length 18;
Best Local Similarity 40.0%; Pred. No. 7.4e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPQNFYKLPQ 10
||| :|:
Db 5 MPHNGCRPPK 14

RESULT 24

Q45615

ID Q45615 PRELIMINARY; PRT; 8 AA.
AC Q45615;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE GutB protein (Fragment).
GN GUTB.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=94253000; PubMed=8195086;
RA Ye R., Wong S.L.;
RT "Transcriptional regulation of the Bacillus subtilis glucitol
RT dehydrogenase gene."
RL J. Bacteriol. 176:3314-3320(1994).
DR EMBL; L16626; AAA20875.1; -.
FT NON TER 8 8
SQ SEQUENCE 8 AA; 927 MW; FD56C772D1A1F1A6 CRC64;

Query Match 30.6%; Score 19; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQN 4
: |||
Db 5 VPQN 8

RESULT 25

Q9HCQ0

ID Q9HCQ0 PRELIMINARY; PRT; 8 AA.
AC Q9HCQ0;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Phosphodiesterase 10A7 (PDE10A7) (Fragment).
GN HSPDE10A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20453115; PubMed=10998054;
RA Fujishige K., Kotera J., Yuasa K., Omori K.;
RT "The human phosphodiesterase PDE10A gene. Genomic organization and
RT evolutionary relatedness with other PDEs containing GAF domains."
RL Eur. J. Biochem. 267:5943-5951(2000).
DR EMBL; AB041779; BAB16368.1; -.
DR GO; GO:0004112; F:cyclic-nucleotide phosphodiesterase activity; NAS.
FT NON TER 8 8
SQ SEQUENCE 8 AA; 966 MW; FD4B19D5A6C76446 CRC64;

Query Match 30.6%; Score 19; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQNF 5
||:|
Db 3 PQSF 6

RESULT 26

Q67605

ID Q67605 PRELIMINARY; PRT; 9 AA.
AC Q67605;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE AL1 protein (Fragment).
GN AL1.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV-R;
RX MEDLINE=91082450; PubMed=1984669;
RA Lazarowitz S.G.;
RT "Molecular characterization of two bipartite geminiviruses causing
RT squash leaf curl disease: Role of viral replication and movement
RT functions in determining host range."
RL Virology 180:70-80(1991).
DR EMBL; M63155; AAA47823.1; -.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1118 MW; 2B30D5B457645417 CRC64;

Query Match 30.6%; Score 19; DB 12; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQN 4
||:|
Db 1 MPRN 4

RESULT 27

Q67606

ID Q67606 PRELIMINARY; PRT; 9 AA.
AC Q67606;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE AL1 protein (Fragment).
GN AL1.
OS Squash leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=10829;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=CV-E;
 RX MEDLINE=91082450; PubMed=1984669;
 RA Lazarowitz S.G.;
 RT "Molecular characterization of two bipartite geminiviruses causing
 RT squash leaf curl disease: Role of viral replication and movement
 RT functions in determining host range.";
 RL Virology 180:70-80(1991).
 DR EMBL; M63157; AAA47822.1; -.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1118 MW; 2B30D5B457645417 CRC64;

Query Match 30.6%; Score 19; DB 12; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQN 4
 ||:
 Db 1 MPRN 4

RESULT 28

Q9URG1

ID Q9URG1 PRELIMINARY; PRT; 11 AA.
 AC Q9URG1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Cytochrome C oxidase subunit 2 (Fragment).
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92035058; PubMed=1657411;
 RA Lemire E.G., Percy J.A., Correia J.M., Crowther B.M., Nargang F.E.;
 RT "Alteration of the cytochrome c oxidase subunit 2 gene in the [exn-5]
 RT mutant of Neurospora crassa.";
 RL Curr. Genet. 20:121-127(1991).
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1222 MW; 936B1558C7605DC5 CRC64;

Query Match 30.6%; Score 19; DB 3; Length 11;
 Best Local Similarity 75.0%; Pred. No. 7e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPQM 11
 :|||
 Db 6 IPQM 9

RESULT 29

Q80GN9

ID Q80GN9 PRELIMINARY; PRT; 11 AA.
 AC Q80GN9;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE C2 orf (Fragment).
 OS Tomato leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=28350;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93174952; PubMed=8438578;
 RA Mullineaux P.M., Rigden J.E., Dry I.B., Krake L.R., Rezaian M.A.;
 RT "Mapping of the polycistronic RNAs of tomato leaf curl geminivirus."
 RL Virology 193:414-423(1993).
 DR EMBL; S55330; AAP13896.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1441 MW; F7588F64C3305AA1 CRC64;

Query Match 30.6%; Score 19; DB 12; Length 11;
 Best Local Similarity 100.0%; Pred. No. 7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NFY 6
 |||
 Db 9 NFY 11

RESULT 30

Q9T4K5

ID Q9T4K5 PRELIMINARY; PRT; 13 AA.
 AC Q9T4K5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE PBSH (Fragment).
 GN PBSH.
 OS Bryopsis sp. C.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpaceae;
 OC Bryopsidaceae; Bryopsis.
 OX NCBI_TaxID=103786;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VARIOUS STRAINS;
 RA Krellwitz E.C., Kowalik K.V., Manos P.S.;
 RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
 RT Atlantic and Caribbean based on Coding and Non-coding sequences of the
 RT Chloroplast psbB Operon."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF170407; AAD56846.1; -.
 DR EMBL; AF170383; AAD56798.1; -.
 DR EMBL; AF170384; AAD56800.1; -.
 DR EMBL; AF170385; AAD56802.1; -.
 DR EMBL; AF170386; AAD56804.1; -.
 DR EMBL; AF170387; AAD56806.1; -.
 DR EMBL; AF170388; AAD56808.1; -.
 DR EMBL; AF170389; AAD56810.1; -.
 DR EMBL; AF170390; AAD56812.1; -.
 DR EMBL; AF170391; AAD56814.1; -.

DR EMBL; AF170392; AAD56816.1; -.
DR EMBL; AF170393; AAD56818.1; -.
DR EMBL; AF170394; AAD56820.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1366 MW; 2C31687A2E93A338 CRC64;

Query Match 30.6%; Score 19; DB 8; Length 13;
Best Local Similarity 75.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQN 4
||:|
Db 1 MPKN 4

RESULT 31

Q9THS3

ID Q9THS3 PRELIMINARY; PRT; 13 AA.
AC Q9THS3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PbsH (Fragment).
GN PBSH.
OS Bryopsis sp. D.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpaceae;
OC Bryopsidaceae; Bryopsis.
OX NCBI_TaxID=103787;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96-21-02;
RA Krellwitz E.C., Kowallik K.V., Manos P.S.;
RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
RT Atlantic and Caribbean based on Coding and Non-coding sequences of the
RT Chloroplast psbB Operon."
RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF170381; AAD56794.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1379 MW; 2C31687A3B73A338 CRC64;

Query Match 30.6%; Score 19; DB 8; Length 13;
Best Local Similarity 75.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQN 4
||:|
Db 1 MPKN 4

RESULT 32

Q9T4K4

ID Q9T4K4 PRELIMINARY; PRT; 13 AA.

AC Q9T4K4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PBSH (Fragment).
GN PBSH.
OS Bryopsis sp. B.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpales;
OC Bryopsidaceae; Bryopsis.
OX NCBI_TaxID=103785;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VARIOUS STRAINS;
RA Krellwitz E.C., Kowallik K.V., Manos P.S.;
RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
RT Atlantic and Caribbean based on Coding and Non-coding sequences of the
RT Chloroplast psbB Operon."
RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF170405; AAD56842.1; -.
DR EMBL; AF170395; AAD56822.1; -.
DR EMBL; AF170396; AAD56824.1; -.
DR EMBL; AF170397; AAD56826.1; -.
DR EMBL; AF170398; AAD56828.1; -.
DR EMBL; AF170399; AAD56830.1; -.
DR EMBL; AF170400; AAD56832.1; -.
DR EMBL; AF170401; AAD56834.1; -.
DR EMBL; AF170402; AAD56836.1; -.
DR EMBL; AF170403; AAD56838.1; -.
DR EMBL; AF170404; AAD56840.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1366 MW; 2C31687A2E93A338 CRC64;

Query Match 30.6%; Score 19; DB 8; Length 13;
Best Local Similarity 75.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQN 4
||:|
Db 1 MPKN 4

RESULT 33

Q9THS2

ID Q9THS2 PRELIMINARY; PRT; 13 AA.
AC Q9THS2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PbsH (Fragment).
GN PBSH.
OS Bryopsis sp. D.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpales;
OC Bryopsidaceae; Bryopsis.

OX NCBI_TaxID=103787;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=97-07-01;
 RA Krellwitz E.C., Kowallik K.V., Manos P.S.;
 RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
 RT Atlantic and Caribbean based on Coding and Non-coding sequences of the
 RT Chloroplast psbB Operon."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF170382; AAD56796.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1366 MW; 2C31687A2E93A338 CRC64;

Query Match 30.6%; Score 19; DB 8; Length 13;
 Best Local Similarity 75.0%; Pred. No. 8.2e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQN 4
 ||:|
 Db 1 MPKN 4

RESULT 34

Q9T4K6

ID Q9T4K6 PRELIMINARY; PRT; 13 AA.
 AC Q9T4K6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE PBSH (Fragment).
 GN PBSH.
 OS Bryopsis sp. A.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpales;
 OC Bryopsidaceae; Bryopsis.
 OX NCBI_TaxID=103784;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VARIOUS STRAINS;
 RA Krellwitz E.C., Kowallik K.V., Manos P.S.;
 RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
 RT Atlantic and Caribbean based on Coding and Non-coding sequences of the
 RT Chloroplast psbB Operon."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF170415; AAD56862.1; -.
 DR EMBL; AF170408; AAD56848.1; -.
 DR EMBL; AF170409; AAD56850.1; -.
 DR EMBL; AF170410; AAD56852.1; -.
 DR EMBL; AF170411; AAD56854.1; -.
 DR EMBL; AF170412; AAD56856.1; -.
 DR EMBL; AF170414; AAD56860.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1366 MW; 2C31687A2E93A338 CRC64;

Query Match 30.6%; Score 19; DB 8; Length 13;
Best Local Similarity 75.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQN 4
||:|
Db 1 MPKN 4

RESULT 35

Q9T4K3

ID Q9T4K3 PRELIMINARY; PRT; 13 AA.
AC Q9T4K3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PBSH (Fragment).
GN PBSH.
OS Bryopsis sp. E.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpaceae;
OC Bryopsidaceae; Bryopsis.
OX NCBI_TaxID=103788;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95-05-03, 96-07-03, 95-12-02, 94-19-1R, 97-13-1R, and 98-08-03;
RA Krellwitz E.C., Kowallik K.V., Manos P.S.;
RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
RT Atlantic and Caribbean based on Coding and Non-coding sequences of the
RT Chloroplast psbB Operon."
RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF170380; AAD56792.1; -.
DR EMBL; AF170373; AAD56778.1; -.
DR EMBL; AF170375; AAD56782.1; -.
DR EMBL; AF170376; AAD56784.1; -.
DR EMBL; AF170377; AAD56786.1; -.
DR EMBL; AF170378; AAD56788.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1366 MW; 2C31687A2E93A338 CRC64;

Query Match 30.6%; Score 19; DB 8; Length 13;
Best Local Similarity 75.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQN 4
||:|
Db 1 MPKN 4

RESULT 36

Q34699

ID Q34699 PRELIMINARY; PRT; 16 AA.
AC Q34699;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cob protein (Fragment).
 GN COB.
 OS Helianthus annuus (Common sunflower).
 OG Mitochondrion.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae;
 OC Helianthus.
 OX NCBI_TaxID=4232;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CMSBASO;
 RA Koehler R.H.;
 RL Submitted (OCT-1991) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; X62592; CAA44477.1; -.
 DR PIR; S22040; S22040.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 1 1
 SQ SEQUENCE 16 AA; 1990 MW; A2980BEE7E26B700 CRC64;

Query Match 30.6%; Score 19; DB 8; Length 16;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NFY 6
 |||
 Db 3 NFY 5

RESULT 37

Q38671

ID Q38671 PRELIMINARY; PRT; 16 AA.
 AC Q38671;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Protein 13 (Fragment).
 OS Bacteriophage P22.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
 OC P22-like viruses.
 OX NCBI_TaxID=10754;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kroeger M., Hobom G.;
 RT "Nucleotide Sequence of PR-operon of P22 is a mosaic of other lambdoid
 RT chromosomes and reveals functional implications for the late gene
 RT expression."
 RL Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86045883; PubMed=2998005;
 RA Renell D., Poteete A.R.;
 RT "Phage P22 lysis genes: Nucleotide sequences and functional
 RT relationships with T4 and lambda genes."

RL Virology 143:280-289(1985).
DR EMBL; X78401; CAA55167.1; -.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1901 MW; B6C364C98EC6D8D2 CRC64;

Query Match 30.6%; Score 19; DB 9; Length 16;
Best Local Similarity 36.4%; Pred. No. 1e+04;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPQNFYKLPQM 11
||: : | |
Db 4 MPEKYDLLTAM 14

RESULT 38

Q13376

ID Q13376 PRELIMINARY; PRT; 17 AA.
AC Q13376;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE RNA binding motif (Fragment).
GN RBM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97032533; PubMed=8875892;
RA Prosser J., Inglis J.D., Condie A., Ma K., Kerr S., Thakrar R.,
RA Taylor K., Cameron J.M., Cooke H.J.;
RT "Degeneracy in human multicopy RBM (YRRM), a candidate spermatogenesis
RT gene.";
RL Mamm. Genome 7:835-842(1996).
DR EMBL; U38450; AAB49815.1; -.
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 2060 MW; 98CD6AEFEC350012 CRC64;

Query Match 30.6%; Score 19; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 QNFYKLPQ 10
| |: ||
Db 10 QAFHLWPQ 17

RESULT 39

Q9XSG1

ID Q9XSG1 PRELIMINARY; PRT; 17 AA.
AC Q9XSG1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE SMCX (Fragment).
GN SMCX.

OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Poloumienko A., Blecher S.;
 RT "Exon-intron structure of SMCX and SMCY genes in bovine and swine."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF135448; AAD34440.1; -.
 FT NON_TER 1 1
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1927 MW; 10351B0D516D16F0 CRC64;

 Query Match 30.6%; Score 19; DB 6; Length 17;
 Best Local Similarity 20.0%; Pred. No. 1.1e+04;
 Matches 2; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

 Qy 1 MPQNFYKLPQ 10
 :|: :: |:
 Db 4 IPKGVWRCPK 13

RESULT 40

Q9PRU8

ID Q9PRU8 PRELIMINARY; PRT; 17 AA.
 AC Q9PRU8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE P130=PHOSPHOPROTEINS TIGHTLY associated with V-CRK in VIVO
 DE (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95105151; PubMed=7806494;
 RA Sakai R., Iwamatsu A., Hirano N., Ogawa S., Tanaka T., Nishida J.,
 RA Yazaki Y., Hirai H.;
 RT "Characterization, partial purification, and peptide sequencing of
 RT p130, the main phosphoprotein associated with v-Crk oncoprotein."
 RL J. Biol. Chem. 269:32740-32746(1994).
 FT NON_TER 1 1
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1861 MW; 379058CDE44F8879 CRC64;

 Query Match 30.6%; Score 19; DB 13; Length 17;
 Best Local Similarity 42.9%; Pred. No. 1.1e+04;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

 Qy 3 QNFYKLP 9
 | |: |

RESULT 41

Q9ZG42

ID Q9ZG42 PRELIMINARY; PRT; 18 AA.
 AC Q9ZG42;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE Proline transport protein (Fragment).
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=L2 434B;
 RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
 RT "Gene identification of Chlamydia trachomatis by random DNA
 RT sequencing.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF087325; AAD04100.1; -.
 FT NON_TER 1 1
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2236 MW; 55C4A82FD42CC261 CRC64;

Query Match 30.6%; Score 19; DB 2; Length 18;
 Best Local Similarity 75.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NFYK 7
 :|||
 Db 9 HFYK 12

RESULT 42

O97773

ID O97773 PRELIMINARY; PRT; 18 AA.
 AC O97773;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE Mibp protein (Fragment).
 GN MIBP.
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bliskovsky V., Zajac K.M.;
 RT "Evolutionary conservation of a 2 kilobase intronic sequence flanking
 RT a tissue specific alternative exon in the mibp gene.";
 RL Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U88970; AAD00667.1; -.
 FT NON_TER 1 1

FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2069 MW; CA377C765AEEEE28A CRC64;

Query Match 30.6%; Score 19; DB 6; Length 18;
Best Local Similarity 42.9%; Pred. No. 1.1e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
||: : |
Db 11 PQSLFTL 17

RESULT 43

Q7YRH7

ID Q7YRH7 PRELIMINARY; PRT; 18 AA.
AC Q7YRH7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NPTB (Fragment).
GN PTBP2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Rahman L., Bliskovski V., Kaye F.J., Zajac-Kaye M.;
RT "Evolutionary conservation of a 2 kilobase intronic sequence flanking
RT a tissue-specific alternative exon in the PTBP2 gene.";
RL Genomics 0:0-0(2003).
DR EMBL; AY333751; AAQ01149.1; -.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2039 MW; 7A6EB521E0C58378 CRC64;

Query Match 30.6%; Score 19; DB 6; Length 18;
Best Local Similarity 42.9%; Pred. No. 1.1e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
||: : |
Db 9 PQSLFTL 15

RESULT 44

Q7TNW8

ID Q7TNW8 PRELIMINARY; PRT; 18 AA.
AC Q7TNW8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NPTB (Fragment).
GN PTBP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RA Rahman L., Bliskovski V., Kaye F.J., Zajac-Kaye M.;
RT "Evolutionary conservation of a 2 kilobase intronic sequence flanking
RT a tissue-specific alternative exon in the PTBP2 gene.";
RL Genomics 0:0-0(2003).
DR EMBL; AY333750; AAQ01148.1; -.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2039 MW; 7A6EB521E0C58378 CRC64;

Query Match 30.6%; Score 19; DB 11; Length 18;
Best Local Similarity 42.9%; Pred. No. 1.1e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
||: : |
Db 9 PQSLFTL 15

RESULT 45

Q7TNW7

ID Q7TNW7 PRELIMINARY; PRT; 18 AA.
AC Q7TNW7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE NPTB (Fragment).
GN PTBP2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Rahman L., Bliskovski V., Kaye F.J., Zajac-Kaye M.;
RT "Evolutionary conservation of a 2 kilobase intronic sequence flanking
RT a tissue-specific alternative exon in the PTBP2 gene.";
RL Genomics 0:0-0(2003).
DR EMBL; AY333752; AAQ01150.1; -.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2039 MW; 7A6EB521E0C58378 CRC64;

Query Match 30.6%; Score 19; DB 11; Length 18;
Best Local Similarity 42.9%; Pred. No. 1.1e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
||: : |
Db 9 PQSLFTL 15

RESULT 46

Q62527

ID Q62527 PRELIMINARY; PRT; 8 AA.
AC Q62527;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Transthyretin (Prealbumin) (Fragment).
GN TTR.
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRET/EI;
RX MEDLINE=94319082; PubMed=8043949;
RA Ko M.S., Wang X., Horton J.H., Hagen M.D., Takahashi N., Maezaki Y.,
RA Nadeau J.H.;
RT "Genetic mapping of 40 cDNA clones on the mouse genome by PCR.";
RL Mamm. Genome 5:349-355(1994).
CC -!- FUNCTION: THYROID HORMONE-BINDING PROTEIN. PROBABLY TRANSPORTS
CC THYROXINE FROM THE BLOODSTREAM TO THE BRAIN.
CC -!- SUBUNIT: HOMOTETRAMER.
DR EMBL; U05689; AAB60461.1; -.
DR PIR; I49404; I49404.
DR MGD; MGI:98865; Ttr.
DR GO; GO:0005615; C:extracellular space; IEA.
DR GO; GO:0019841; F:retinol binding; IEA.
DR GO; GO:0006590; P:thyroid hormone generation; IEA.
DR GO; GO:0006810; P:transport; IEA.
KW Transport; Retinol-binding; Vitamin A; Thyroid hormone.
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 828 MW; 9156C76455A2D2CD CRC64;

Query Match 29.0%; Score 18; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PQN 4
|||
Db 6 PQN 8

RESULT 47

Q94VG2

ID Q94VG2 PRELIMINARY; PRT; 9 AA.
AC Q94VG2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COI.
OS Varanus indicus (Mangrove monitor).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=62043;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL; AF407505; AAL10069.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1258 MW; 881259C727336411 CRC64;

Query Match 29.0%; Score 18; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FYK 7
 |||
 Db 7 FYK 9

RESULT 48

Q9S8J8

ID Q9S8J8 PRELIMINARY; PRT; 9 AA.
 AC Q9S8J8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE ORYZATENSIN=BIOACTIVE peptide.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95102521; PubMed=7804141;
 RA Takahashi M., Moriguchi S., Yoshikawa M., Sasaki R.;
 RT "Isolation and characterization of oryzatensin: a novel bioactive
 RT peptide with ileum-contracting and immunomodulating activities derived
 RT from rice albumin."
 RL Biochem. Mol. Biol. Int. 33:1151-1158(1994).
 DR Gramene; Q9S8J8; -.
 SQ SEQUENCE 9 AA; 1093 MW; 0E8C67377B56877B CRC64;

Query Match 29.0%; Score 18; DB 10; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1e+06;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 YKLPQ 10
 | ||:
 Db 5 YPLPR 9

RESULT 49

Q9H121

ID Q9H121 PRELIMINARY; PRT; 10 AA.
 AC Q9H121;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE DJ309F20.1.2 (Isoform 2 of guanine nucleotide binding protein (G
 DE protein), alpha stimulating activity polypeptide 1) (Fragment).
 GN GNAS1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Laird G.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AL121917; CAC18783.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 10 AA; 1095 MW; 7809E3D322C7244B CRC64;

Query Match 29.0%; Score 18; DB 4; Length 10;
 Best Local Similarity 42.9%; Pred. No. 9.7e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 QNFYKLP 9
 :| | |
 Db 3 ENLVKAP 9

RESULT 50

Q14462

ID Q14462 PRELIMINARY; PRT; 13 AA.
 AC Q14462;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Glycophorin St-a (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90264417; PubMed=1971625;
 RA Rearden A., Phan H., Dubnicoff T., Kudo S., Fukuda M.;
 RT "Identification of the crossing-over point of a hybrid gene encoding
 RT human glycophorin variant St-a: Similarity to the crossing-over point
 RT in haptoglobin-related genes."
 RL J. Biol. Chem. 265:9259-9263(1990).
 DR EMBL; M33507; AAA35942.1; -.
 DR PIR; I70076; I70076.
 FT NON_TER 1 1
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1489 MW; 466C6DF642414767 CRC64;

Query Match 29.0%; Score 18; DB 4; Length 13;
 Best Local Similarity 75.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 YKLP 9
 | ||
Db 4 YNLP 7

Search completed: July 4, 2004, 04:45:38
Job time : 21.7164 secs

OM protein - protein search, using sw model

Run on: July 4, 2004, 04:33:26 ; Search time 3.77612 Seconds
 (without alignments)
 151.683 Million cell updates/sec

Title: US-09-641-802-6
 Perfect score: 62
 Sequence: 1 MPQNFYKLPQM 11

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 952

Minimum DB seq length: 7
 Maximum DB seq length: 18

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 100 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	26	41.9	15	1	SODM_ENTAE	P22799 enterobacte
2	24	38.7	11	1	TKNA_RANRI	P29207 rana ridibu
3	23	37.1	11	1	TKN2_UPERU	P08616 uperoleia r
4	23	37.1	11	1	TKNA_CHICK	P19850 gallus gall
5	23	37.1	11	1	TKNA_HORSE	P01290 equus cabal
6	22	35.5	11	1	TKNA_RANCA	P22688 rana catesb
7	22	35.5	11	1	TKND_RANCA	P22691 rana catesb
8	22	35.5	11	1	TKN_PHYFU	P08615 physalaemus
9	21	33.9	16	1	BRB_BASAL	P83187 basella alb
10	20	32.3	7	1	FARB_CALVO	P41866 calliphora
11	20	32.3	9	1	TKL1_LOCFI	P16223 locusta mig
12	20	32.3	11	1	TKN1_UPEIN	P82026 uperoleia i
13	20	32.3	11	1	TKN1_UPERU	P08612 uperoleia r
14	20	32.3	12	1	TKN2_KASMA	P08614 kassina mac
15	19	30.6	11	1	TKNA_GADMO	P28498 gadus morhu
16	19	30.6	13	1	UN02_PINPS	P81667 pinus pinas
17	19	30.6	15	1	LEC2_PSOSC	P22585 psophocarpu

18	19	30.6	15	1	SODM_STRGR	P80733	streptomyce
19	19	30.6	18	1	A2M_OCTVU	P30800	octopus vul
20	19	30.6	18	1	SODM_MYCHA	P80582	mycobacteri
21	18	29.0	8	1	NPMB_BOVIN	P15507	bos taurus
22	18	29.0	11	1	TKN4_PSEGU	P42989	pseudophryn
23	18	29.0	11	1	TKN5_PSEGU	P42990	pseudophryn
24	18	29.0	11	1	TKNA_ONCMY	P28499	oncorhynchu
25	18	29.0	15	1	AFP3_MALPA	P83137	malva parvi
26	18	29.0	16	1	PA2_NAJSP	Q10756	naja sputat
27	18	29.0	17	1	BTID_BOOMI	P83607	boophilus m
28	18	29.0	18	1	NPMA_BOVIN	P15506	bos taurus
29	17	27.4	9	1	TKC1_CALVO	P41517	calliphora
30	17	27.4	10	1	FAR6_PANRE	P82660	panagrellus
31	17	27.4	15	1	CKX_WHEAT	P58763	triticum ae
32	17	27.4	18	1	FMF1_ECOLI	P20860	escherichia
33	17	27.4	18	1	HEMH_THETS	P80155	theromyzon
34	17	27.4	18	1	LUXB_KRYAS	P18300	kryptophana
35	16	25.8	9	1	BUK_CLOPA	P81337	clostridium
36	16	25.8	9	1	HUTU_KLEAE	P12381	klebsiella
37	16	25.8	10	1	CATB_SHEEP	P83205	ovis aries
38	16	25.8	10	1	TKNB_RANCA	P22689	rana catesb
39	16	25.8	11	1	CXLI_CONMR	P58807	conus marmo
40	16	25.8	11	1	TKNA_SCYCA	P41333	scyliorhinu
41	16	25.8	12	1	PPK4_PERAM	P82619	periplaneta
42	16	25.8	13	1	CRTC_RANES	P31832	rana escule
43	16	25.8	13	1	CXL4_CONMR	P58810	conus marmo
44	16	25.8	14	1	SMS1_MYOSC	P20750	myoxocephal
45	16	25.8	14	1	SMS_ALLMI	P31885	alligator m
46	16	25.8	14	1	TKNM_RANMA	P40951	rana margar
47	16	25.8	15	1	GTS_ASADI	P83246	asaphis dic
48	16	25.8	15	1	LEC1_PSOSC	P22582	psophocarpu
49	16	25.8	15	1	MCA2_RHOOP	P56870	rhodococcus
50	16	25.8	16	1	AF1S_MALPA	P83140	malva parvi
51	15	24.2	10	1	TKN1_SCYCA	P08608	scyliorhinu
52	15	24.2	10	1	TKS1_AEDAE	P42634	aedes aegyp
53	15	24.2	10	1	TKS2_AEDAE	P42635	aedes aegyp
54	15	24.2	11	1	TIN4_HOPTI	P82654	hoplobatrac
55	15	24.2	12	1	RF1_CONSP	P58805	conus spuri
56	15	24.2	12	1	TA10_TREME	P01371	tremella me
57	15	24.2	12	1	TIN3_HOPTI	P82653	hoplobatrac
58	15	24.2	13	1	SODM_CANFA	P54712	canis famil
59	15	24.2	13	1	YPNP_PHOLU	P41122	photorhabdu
60	15	24.2	14	1	LECB_PSOSC	P22584	psophocarpu
61	15	24.2	14	1	SODN_STRGR	P80732	streptomyce
62	15	24.2	15	1	AF1L_MALPA	P83141	malva parvi
63	15	24.2	15	1	AVP2_CAVPO	P83508	cavia porce
64	15	24.2	15	1	CBPB_PROAT	P19628	protopterus
65	15	24.2	15	1	IRBP_CRISP	P12665	cricetidae
66	15	24.2	15	1	LEC3_PSOSC	P22583	psophocarpu
67	15	24.2	15	1	LPF_ECOLI	P03057	escherichia
68	15	24.2	16	1	AF2S_MALPA	P83142	malva parvi
69	15	24.2	16	1	HP29_SARPE	P29184	sarcophaga
70	15	24.2	18	1	YPE4_LACLC	P42022	lactococcus
71	14.5	23.4	10	1	TKL3_LOCM1	P30249	locusta mig
72	14.5	23.4	15	1	DCMM_PSECH	P19917	pseudomonas
73	14	22.6	7	1	FAR1_MACRS	P83274	macrobrachi
74	14	22.6	7	1	FAR1_PROCL	P38499	procambarus

75	14	22.6	7	1	FAR2_PROCL	P38498	procambarus
76	14	22.6	8	1	FAR1_PENMO	P83316	penaeus mon
77	14	22.6	8	1	FAR2_MACRS	P83275	macrobrachi
78	14	22.6	8	1	FAR3_HOMAM	P41486	homarus ame
79	14	22.6	8	1	FAR4_HOMAM	P41487	homarus ame
80	14	22.6	8	1	LCK8_LEUMA	P19990	leucophaea
81	14	22.6	8	1	UC26_MAIZE	P80632	zea mays (m
82	14	22.6	9	1	D1_NEPNO	P24816	nephrops no
83	14	22.6	9	1	FAR3_MACRS	P83276	macrobrachi
84	14	22.6	9	1	FAR6_MACRS	P83279	macrobrachi
85	14	22.6	9	1	NEUU_CAVPO	P34966	cavia porce
86	14	22.6	10	1	AL19_CARMA	P81822	carcinus ma
87	14	22.6	10	1	FAR7_MACRS	P83280	macrobrachi
88	14	22.6	10	1	TKNC_RANCA	P22690	rana catesb
89	14	22.6	10	1	TKN_PHYBI	P08610	phyllomedus
90	14	22.6	10	1	URA7_HUMAN	P34990	homo sapien
91	14	22.6	11	1	BPPB_AGKHA	P01021	agkistrodon
92	14	22.6	11	1	TKN1_PSEGU	P42986	pseudophryn
93	14	22.6	11	1	TKN2_PSEGU	P42987	pseudophryn
94	14	22.6	11	1	TKN3_PSEGU	P42988	pseudophryn
95	14	22.6	12	1	FAR7_PENMO	P83322	penaeus mon
96	14	22.6	12	1	GRAR_RANRU	P40754	rana rugosa
97	14	22.6	12	1	TKN1_KASMA	P08613	kassina mac
98	14	22.6	13	1	CRTC_BOVIN	P28489	bos taurus
99	14	22.6	13	1	MP1_MICOC	P81532	microplitis
100	14	22.6	15	1	FGF1_CANFA	P18651	canis famil

ALIGNMENTS

RESULT 1

SODM_ENTAE

ID SODM_ENTAE STANDARD; PRT; 15 AA.
AC P22799;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Fe] (EC 1.15.1.1) (Fragment).
GN SODA.
OS Enterobacter aerogenes (Aerobacter aerogenes).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Enterobacter.
OX NCBI_TaxID=548;
RN [1]
RP SEQUENCE.
RX MEDLINE=91248479; PubMed=1368658;
RA Kim S.W., Lee S.O., Lee T.H.;
RT "Purification and characterization of superoxide dismutase from
RT Aerobacter aerogenes.";
RL Agric. Biol. Chem. 55:101-108(1991).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 iron ion per subunit (By similarity).
CC -!- SUBUNIT: Homodimer.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase

CC family.
 DR PIR; PN0615; PN0615.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe; 1.
 DR PROSITE; PS00088; SOD_MN; PARTIAL.
 KW Oxidoreductase; Metal-binding; Iron.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1756 MW; 352F3D949202E642 CRC64;

Query Match 41.9%; Score 26; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 65;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YKLPQM 11
 |:|:|:
 Db 2 YELPQL 7

RESULT 2

TKNA_RANRI
 ID TKNA_RANRI STANDARD; PRT; 11 AA.
 AC P29207;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranakinin (Substance-P-related peptide).
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92044543; PubMed=1658233;
 RA O'Harte F., Burcher E., Lovas S., Smith D.D., Vaudry H., Conlon J.M.;
 RT "Ranakinin: a novel NK1 tachykinin receptor agonist isolated with
 RT neurokinin B from the brain of the frog Rana ridibunda.";
 RL J. Neurochem. 57:2086-2091(1991).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1352 MW; 3A2460CC59D40B07 CRC64;

Query Match 38.7%; Score 24; DB 1; Length 11;
 Best Local Similarity 57.1%; Pred. No. 1.1e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
|: || |
Db 4 PERFYGL 10

RESULT 3

TKN2_UPERU

ID TKN2_UPERU STANDARD; PRT; 11 AA.
AC P08616;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Rugosauperolein II ([Lys5,Thr6]physalaemin).
OS Uperoleia rugosa (Wrinkled toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=8368;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=80223080; PubMed=7389029;
RA Nakajima T., Yasuhara T., Erspamer V., Erspamer G.F., Negri L.;
RT "Physalaemin- and bombesin-like peptides in the skin of the
RT Australian leptodactylid frog Uperoleia rugosa.";
RL Chem. Pharm. Bull. 28:689-695(1980).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1270 MW; 3293693E59D1A327 CRC64;

Query Match 37.1%; Score 23; DB 1; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
|: || |
Db 4 PKTFYGL 10

RESULT 4

TKNA_CHICK

ID TKNA_CHICK STANDARD; PRT; 11 AA.
AC P19850;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=88204263; PubMed=2452461;
 RA Conlon J.M., Katsoulis S., Schmidt W.E., Thim L.;
 RT "[Arg3]substance P and neurokinin A from chicken small intestine.";
 RL Regul. Pept. 20:171-180(1988).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; JN0023; JN0023.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1377 MW; 21487FE3C9D6C6C7 CRC64;

Query Match 37.1%; Score 23; DB 1; Length 11;
 Best Local Similarity 57.1%; Pred. No. 1.7e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
 |||:|
 Db 4 PQQFFGL 10

RESULT 5

TKNA_HORSE
 ID TKNA_HORSE STANDARD; PRT; 11 AA.
 AC P01290;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 GN TAC1 OR NKNA OR TAC2 OR NKA.
 OS Equus caballus (Horse), and
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796, 10141;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Horse;
 RA Studer R.O., Trzeciak A., Lergier W.;
 RT "Isolation and amino-acid sequence of substance P from horse
 RT intestine.";

RL Helv. Chim. Acta 56:860-866(1973).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=C.porcellus;
 RX MEDLINE=90044685; PubMed=2478925;
 RA Murphy R.;
 RT "Primary amino acid sequence of guinea-pig substance P.";
 RL Neuropeptides 14:105-110(1989).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; A01558; SPHO.
 DR PIR; A60654; A60654.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1349 MW; 3E757FE3C9D6C6C7 CRC64;

Query Match 37.1%; Score 23; DB 1; Length 11;
 Best Local Similarity 57.1%; Pred. No. 1.7e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
 || |: |
 Db 4 PQQFFGL 10

RESULT 6

TKNA_RANCA
 ID TKNA_RANCA STANDARD; PRT; 11 AA.
 AC P22688;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranatachykinin A (RTK A).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain, and Intestine;
 RX MEDLINE=91254337; PubMed=2043143;
 RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
 RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
 RT brain and intestine.";
 RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Intestine;

RX MEDLINE=94023216; PubMed=8210506;
 RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
 RT "Four novel tachykinins in frog (*Rana catesbeiana*) brain and
 RT intestine.";
 RL Regul. Pept. 46:81-88(1993).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; A61033; A61033.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1311 MW; 200D60CC59D40AB7 CRC64;

 Query Match 35.5%; Score 22; DB 1; Length 11;
 Best Local Similarity 57.1%; Pred. No. 2.6e+02;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

 Qy 2 PQNFYKL 8
 | |||
 Db 4 PDRFYGL 10

RESULT 7

TKND_RANCA
 ID TKND_RANCA STANDARD; PRT; 11 AA.
 AC P22691;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranatachykinin D (RTK D).
 OS *Rana catesbeiana* (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; *Rana*.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Intestine;
 RX MEDLINE=91254337; PubMed=2043143;
 RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
 RT "Isolation of four novel tachykinins from frog (*Rana catesbeiana*)
 RT brain and intestine.";
 RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=94023216; PubMed=8210506;
 RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
 RT "Four novel tachykinins in frog (*Rana catesbeiana*) brain and
 RT intestine.";

RL Regul. Pept. 46:81-88(1993).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; D61033; D61033.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR PROSITE; PS00267; TACHYKININ; FALSE_NEG.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1350 MW; 3A34256C59D40B07 CRC64;

Query Match 35.5%; Score 22; DB 1; Length 11;
 Best Local Similarity 60.0%; Pred. No. 2.6e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PQNFY 6
 | : ||
 Db 4 PERFY 8

RESULT 8

TKN_PHYFU
 ID TKN_PHYFU STANDARD; PRT; 11 AA.
 AC P08615;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Physalaemin.
 OS Physalaemus fuscumaculatus (Neotropical frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Leptodactylidae;
 OC Leptodactylinae; Physalaemus.
 OX NCBI_TaxID=8378;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=66076612; PubMed=5857249;
 RA Erspamer V., Anastasi A., Bertaccini G., Cei J.M.;
 RT "Structure and pharmacological actions of physalaemin, the main
 RT active polypeptide of the skin of Physalaemus fuscumaculatus.";
 RL Experientia 20:489-490(1964).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S07201; S07201.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1283 MW; 3293693E59C33457 CRC64;

Query Match 35.5%; Score 22; DB 1; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PQNFYKL 8
| |||
Db 4 PNKFYGL 10

RESULT 9

BRB_BASAL

ID BRB_BASAL STANDARD; PRT; 16 AA.
AC P83187;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-basrubin (Fragment).
OS Basella alba (Malabar spinach) (Ceylon spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Basellaceae; Basella.
OX NCBI_TaxID=3589;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Seed;
RX MEDLINE=21547763; PubMed=11688973;
RA Wang H., Ng T.B.;
RT "Novel antifungal peptides from ceylon spinach seeds.";
RL Biochem. Biophys. Res. Commun. 288:765-770(2001).
CC -!- FUNCTION: Possesses antifungal activity against B.cinerea,
CC M.arachidicola and F.oxysporum but not C.comatus and R.solani.
CC Inhibits HIV-1 reverse transcriptase and cell-free translation.
DR GO; GO:0003799; F:antifungal peptide activity; IDA.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; IDA.
KW Fungicide.
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1952 MW; 28F9FE4FC181682C CRC64;

Query Match 33.9%; Score 21; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 6e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PQNFYK 7
| ||:
Db 6 PSKFYE 11

RESULT 10

FARB_CALVO

ID FARB_CALVO STANDARD; PRT; 7 AA.
AC P41866;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE CalliFMRFamide 11.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Thoracic ganglion;
 RX MEDLINE=92196111; PubMed=1549595;
 RA Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 RT neuropeptides (designated calliFMRFamides) from the blowfly
 RT Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 CC family.
 DR PIR; B44787; B44787.
 KW Neuropeptide; Amidation.
 FT MOD_RES 7 7 AMIDATION.
 SQ SEQUENCE 7 AA; 926 MW; 69D40699C44AB700 CRC64;

Query Match 32.3%; Score 20; DB 1; Length 7;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYK 7
 | || :
 Db 1 PDNFMR 6

RESULT 11

TKL1_LOCMI

ID TKL1_LOCMI STANDARD; PRT; 9 AA.

AC P16223;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Locustatachykinin I (TK-I).

OS Locusta migratoria (Migratory locust).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;

OC Acridoidea; Acrididae; Oedipodinae; Locusta.

OX NCBI_TaxID=7004;

RN [1]

RP SEQUENCE.

RC TISSUE=Brain;

RX MEDLINE=90184489; PubMed=2311766;

RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;

RT "Locustatachykinin I and II, two novel insect neuropeptides with
 RT homology to peptides of the vertebrate tachykinin family.";

RL FEBS Lett. 261:397-401(1990).

CC -!- FUNCTION: Myoactive peptide. Stimulates the contraction of the
 CC oviduct and foregut.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 DR PIR; S08265; ECLQ1M.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 939 MW; 2389C86B59C865A7 CRC64;

Query Match 32.3%; Score 20; DB 1; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFY 6
 | |
 Db 2 PSGFY 6

RESULT 12

TKN1_UPEIN

ID TKN1_UPEIN STANDARD; PRT; 11 AA.
 AC P82026;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Uperin 1.1.
 OS Uperoleia inundata (Floodplain toadlet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=104953;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
 RA Adams G.W., Severini C.;
 RT "Novel uperin peptides from the dorsal glands of the australian
 RT floodplain toadlet Uperoleia inundata.";
 RL Aust. J. Chem. 49:475-484(1996).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=1208; METHOD=FAB.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11 AMIDATION.
 SQ SEQUENCE 11 AA; 1226 MW; 3293693E59CDD457 CRC64;

Query Match 32.3%; Score 20; DB 1; Length 11;
 Best Local Similarity 57.1%; Pred. No. 6.2e+02;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
| |||
Db 4 PNAFYGL 10

RESULT 13

TKN1_UPERU

ID TKN1_UPERU STANDARD; PRT; 11 AA.
AC P08612;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Uperolein.
OS Uperoleia rugosa (Wrinkled toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=8368;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=75131227; PubMed=1120493;
RA Anastasi A., Erspamer V., Endean R.;
RT "Structure of uperolein, a physalaemin-like endecapeptide occurring
RT in the skin of Uperoleia rugosa and Uperoleia marmorata.";
RL Experientia 31:394-395(1975).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1252 MW; 32867C3E59CDD457 CRC64;

Query Match 32.3%; Score 20; DB 1; Length 11;
Best Local Similarity 57.1%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
| |||
Db 4 PNAFYGL 10

RESULT 14

TKN2_KASMA

ID TKN2_KASMA STANDARD; PRT; 12 AA.
AC P08614;

DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hylambatin.
 OS *Kassina maculata* (African rhacophorid frog) (*Hylambates maculatus*).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Hyperoliidae;
 OC *Kassina*.
 OX NCBI_TaxID=8414;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Yasuhara T., Nakajima T., Erspamer G.F., Erspamer V.;
 RT "New tachykinins, Glu2, Pro5-kassinin (hylambates-kassinin) and
 RT hylambatin, in the skin of the African rhacophorid frog *Hylambates*
 RT *maculatus*.";
 RL Biomed. Res. 2:613-617(1981).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S07436; S07436.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 12 12 AMIDATION.
 SQ SEQUENCE 12 AA; 1441 MW; 3287CD2F0DD40AB7 CRC64;

Query Match 32.3%; Score 20; DB 1; Length 12;
 Best Local Similarity 60.0%; Pred. No. 6.8e+02;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFY 6
 | ||
 Db 5 PDRFY 9

RESULT 15

TKNA_GADMO

ID TKNA_GADMO STANDARD; PRT; 11 AA.
 AC P28498;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS *Gadus morhua* (Atlantic cod).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; *Gadus*.
 OX NCBI_TaxID=8049;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;

RX MEDLINE=92298992; PubMed=1376687;
 RA Jensen J., Conlon J.M.;
 RT "Substance-P-related and neurokinin-A-related peptides from the brain
 RT of the cod and trout.";
 RL Eur. J. Biochem. 206:659-664(1992).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S23306; S23306.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
 SQ SEQUENCE 11 AA; 1315 MW; 214860D759D6C6C7 CRC64;

Query Match 30.6%; Score 19; DB 1; Length 11;
 Best Local Similarity 57.1%; Pred. No. 9.5e+02;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
 ||| |
 Db 4 PQQFIGL 10

RESULT 16

UN02_PINPS

ID UN02_PINPS STANDARD; PRT; 13 AA.
 AC P81667;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of needles (N55) (Fragments).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 RT proteins.";
 RL Electrophoresis 20:1098-1108(1999).
 CC -!- INDUCTION: By water stress.
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 5.4, its MW is: 43 kDa.
 FT NON_TER 1 1
 FT NON_CONS 7 8
 FT NON_TER 13 13

SQ SEQUENCE 13 AA; 1559 MW; 966B5A43EF94B411 CRC64;

Query Match 30.6%; Score 19; DB 1; Length 13;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 FYKLP 9

|||

Db 1 FYSAP 5

RESULT 17

LEC2_PSOSC

ID LEC2_PSOSC STANDARD; PRT; 15 AA.
AC P22585;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Basic lectin B2 (Fragment).
OS Psophocarpus scandens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Psophocarpus.
OX NCBI_TaxID=3890;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RA Kortt A.A.;
RT "Isolation and characterization of the lectins from the seeds of
RT Psophocarpus scandens.";
RL Phytochemistry 27:2847-2855(1988).
CC -!- SUBUNIT: DIMER OF TWO IDENTICAL OR NEARLY IDENTICAL SUBUNITS OF
CC ABOUT 32000 APPARENT MW.
CC -!- PTM: CONTAINS ABOUT 9% CARBOHYDRATE. HETEROGENEITY IN CARBOHYDRATE
CC COMPOSITION MAY RESULT IN DIFFERENT ISOLECTIN FORMS.
CC -!- SIMILARITY: WITH P.TETRAGONOLOBUS BASIC LECTINS IN N-TERMINAL
CC SEQUENCE, AA COMPOSITION, ERYTHROCYTE AND SUGAR SPECIFICITIES.
DR PIR; PA0008; PA0008.
KW Lectin; Glycoprotein.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1847 MW; D194CE400C832796 CRC64;

Query Match 30.6%; Score 19; DB 1; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 NFYKLPQ 10

|||

Db 7 NFNKFEQ 13

RESULT 18

SODM_STRGR

ID SODM_STRGR STANDARD; PRT; 15 AA.
AC P80733;
DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Superoxide dismutase [Fe-Zn] (EC 1.15.1.1) (Fragment).
 GN SOD2.
 OS *Streptomyces griseus*.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1911;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=KCTC 9006;
 RX MEDLINE=97056064; PubMed=8900409;
 RA Youn H.-D., Youn H., Lee J.-W., Yim Y.-I., Lee J.K., Hah Y.C.,
 RA Kang S.-O.;
 RT "Unique isozymes of superoxide dismutase in *Streptomyces griseus*."
 RL Arch. Biochem. Biophys. 334:341-348(1996).
 CC -!- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -!- COFACTOR: Binds 1 iron or zinc ion per subunit (By similarity).
 CC -!- SUBUNIT: Tetramer.
 CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
 CC family.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe; 1.
 DR PROSITE; PS00088; SOD_MN; PARTIAL.
 KW Oxidoreductase; Metal-binding; Iron; Zinc.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1685 MW; 327993F710861372 CRC64;

Query Match 30.6%; Score 19; DB 1; Length 15;
 Best Local Similarity 60.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 YKLPQ 10
 | ||:
 Db 3 YTLPE 7

RESULT 19

A2M OCTVU

ID A2M_OCTVU STANDARD; PRT; 18 AA.
 AC P30800;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Alpha-2-macroglobulin homolog (Alpha-2-M) (Fragment).
 OS *Octopus vulgaris* (Octopus).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.
 OX NCBI_TaxID=6645;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92344633; PubMed=1379044;
 RA Thøgersen I.B., Salvesen G., Brucato F.H., Pizzo S.V., Enghild J.J.;
 RT "Purification and characterization of an alpha-macroglobulin
 RT proteinase inhibitor from the mollusc *Octopus vulgaris*.";

RL Biochem. J. 285:521-527(1992).
 CC -!- FUNCTION: Is able to inhibit all four classes of proteinases by a
 CC unique "trapping" mechanism. This protein has a peptide stretch,
 CC called the 'bait region' which contains specific cleavage sites
 CC for different proteinases. When a proteinase cleaves the bait
 CC region, a conformational change is induced in the protein which
 CC traps the proteinase. The entrapped enzyme remains active against
 CC low molecular weight substrates (activity against high molecular
 CC weight substrates is greatly reduced). Following cleavage in the
 CC bait region a thioester bond is hydrolyzed and mediates the
 CC covalent binding of the protein to the proteinase.
 CC -!- SUBUNIT: Homodimer; disulfide-linked.
 CC -!- SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACROGLOBULIN FAMILY,
 CC INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.
 DR PIR; S23971; S23971.
 DR GO; GO:0004866; F:endorpeptidase inhibitor activity; NAS.
 DR InterPro; IPR001599; MacrogloblnA2.
 DR InterPro; IPR008930; Terp_cyc_toroid.
 DR Pfam; PF00207; A2M; 1.
 DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
 KW Serine protease inhibitor; Glycoprotein; Plasma; Bait region;
 KW Thioester bond.
 FT NON_TER 1 1
 FT CROSSLNK 5 8 Isoglutamyl cysteine thioester (Cys-Gln).
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 2011 MW; D8D61C473D901C9D CRC64;

 Query Match 30.6%; Score 19; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 4 NFY 6
 |||
 Db 12 NFY 14

RESULT 20
 SODM_MYCHA
 ID SODM_MYCHA STANDARD; PRT; 18 AA.
 AC P80582;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Superoxide dismutase [Mn] (EC 1.15.1.1) (Fragment).
 GN SODA OR SOD.
 OS Mycobacterium habana.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1784;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=TMC 5135;
 RX MEDLINE=96262709; PubMed=8704977;
 RA Bisht D., Mehrotra J., Dhindsa M.S., Singh N.B., Sinha S.;
 RT "A major T-cell-inducing cytosolic 23 kDa protein antigen of the
 RT vaccine candidate Mycobacterium habana is superoxide dismutase.";
 RL Microbiology 142:1375-1383(1996).

CC -!- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -!- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
 CC -!- SUBUNIT: Homodimer (Probable).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
 CC family.
 DR InterPro; IPR001189; SODismutase.
 DR Pfam; PF00081; sodfe; 1.
 DR PROSITE; PS00088; SOD_MN; PARTIAL.
 KW Oxidoreductase; Metal-binding; Manganese.
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 1883 MW; A4161A3DAC93F710 CRC64;

Query Match 30.6%; Score 19; DB 1; Length 18;
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 YKLPQM 11
 | | | :
 Db 3 YTL PDL 8

RESULT 21

NPMB_BOVIN

ID NPMB_BOVIN STANDARD; PRT; 8 AA.
 AC P15507;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Morphine modulating neuropeptide B.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain;
 RX MEDLINE=86067985; PubMed=3865193;
 RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
 RT "Isolation, sequencing, synthesis, and pharmacological
 RT characterization of two brain neuropeptides that modulate the action
 RT of morphine."
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
 CC -!- FUNCTION: Modulates the action of morphine.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 DR PIR; B24749; B24749.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 1082 MW; 87D416C776D9C729 CRC64;

Query Match 29.0%; Score 18; DB 1; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PQNF 5
|||
Db 5 PQRF 8

RESULT 22

TKN4_PSEGU

ID TKN4_PSEGU STANDARD; PRT; 11 AA.
AC P42989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide I (PG-SPI).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guentheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; E60409; E60409.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1294 MW; 3A247C2CC9CB1AB7 CRC64;

Query Match 29.0%; Score 18; DB 1; Length 11;
Best Local Similarity 42.9%; Pred. No. 1.4e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
| |:
Db 4 PDEFFGL 10

RESULT 23

TKN5_PSEGU

ID TKN5_PSEGU STANDARD; PRT; 11 AA.
AC P42990;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P-like peptide II (PG-SPII).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simmaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Erspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RT the Australian frog Pseudophryne guntheri.";
RL Peptides 11:299-304(1990).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; F60409; F60409.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR InterPro; IPR008215; Tachykinin.
DR Pfam; PF02202; Tachykinin; 1.
DR SMART; SM00203; TK; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1293 MW; 3A247C2CC9CB1457 CRC64;

Query Match 29.0%; Score 18; DB 1; Length 11;
Best Local Similarity 42.9%; Pred. No. 1.4e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
| |:
Db 4 PNEFFGL 10

RESULT 24

TKNA_ONCMY
ID TKNA_ONCMY STANDARD; PRT; 11 AA.
AC P28499;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Substance P.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=92298992; PubMed=1376687;
 RA Jensen J., Conlon J.M.;
 RT "Substance-P-related and neurokinin-A-related peptides from the brain
 RT of the cod and trout.";
 RL Eur. J. Biochem. 206:659-664(1992).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; S23308; S23308.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR InterPro; IPR008215; Tachykinin.
 DR Pfam; PF02202; Tachykinin; 1.
 DR SMART; SM00203; TK; 1.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
 FT MOD_RES 11 11 AMIDATION (BY SIMILARITY).
 SQ SEQUENCE 11 AA; 1358 MW; 214860DEC9D6D1F7 CRC64;

Query Match 29.0%; Score 18; DB 1; Length 11;
 Best Local Similarity 42.9%; Pred. No. 1.4e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
 | |:
 Db 4 PHQFFGL 10

RESULT 25

AFP3_MALPA

ID AFP3_MALPA STANDARD; PRT; 15 AA.
 AC P83137;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Antifungal protein 3 (CW-3) (Fragment).
 OS Malva parviflora (Little mallow) (Cheeseweed).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Malva.
 OX NCBI_TaxID=145753;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=Seed;
 RX MEDLINE=21199399; PubMed=11302747;
 RA Wang X., Bunkers G.J., Walters M.R., Thoma R.S.;
 RT "Purification and characterization of three antifungal proteins from
 RT cheeseweed (Malva parviflora).";

RL Biochem. Biophys. Res. Commun. 282:1224-1228(2001).
 CC -!- FUNCTION: Possesses antifungal activity against P.infestans but
 CC not F.graminearum.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt
 CC concentration.
 DR GO; GO:0003799; F:antifungal peptide activity; IDA.
 DR GO; GO:0007275; P:development; NAS.
 KW Fungicide; Antibiotic.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 2016 MW; 01D9CA069F1A52DB CRC64;

Query Match 29.0%; Score 18; DB 1; Length 15;
 Best Local Similarity 44.4%; Pred. No. 2e+03;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 PQNFYKLPQ 10
 || |: |
 Db 4 PQRRYQEEQ 12

RESULT 26

PA2_NAJSP

ID PA2_NAJSP STANDARD; PRT; 16 AA.
 AC Q10756;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase)
 DE (Muscarinic inhibitor) (Fragment).
 OS Naja sputatrix (Malayan spitting cobra).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Elapinae; Naja.
 OX NCBI_TaxID=33626;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=96195757; PubMed=8638927;
 RA Miyoshi S.-I., Tu A.T.;
 RT "Phospholipase A2 from Naja naja sputatrix venom is a muscarinic
 RT acetylcholine receptor inhibitor."
 RL Arch. Biochem. Biophys. 328:17-25(1996).
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
 CC acyl groups in 3-sn-phosphoglycerides. Blocks neuromuscular
 CC transmission at the postsynaptic site. Binds to the muscarinic
 CC acetylcholine receptor.
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 CC acylglycerophosphocholine + a fatty acid anion.
 CC -!- COFACTOR: Binds 1 calcium ion (By similarity).
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group I
 CC subfamily.
 DR PIR; S65520; S65520.
 DR HSSP; P00598; 1POA.
 DR InterPro; IPR001211; PhospholipaseA2.

DR Pfam; PF00068; phoslip; 1.
 DR PROSITE; PS00119; PA2_ASP; PARTIAL.
 DR PROSITE; PS00118; PA2_HIS; PARTIAL.
 KW Hydrolase; Lipid degradation; Calcium; Toxin; Neurotoxin;
 KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor.
 FT NON_TER 16 16
 SQ SEQUENCE 16 AA; 1969 MW; 9AC1F9834BB585F0 CRC64;

Query Match 29.0%; Score 18; DB 1; Length 16;
 Best Local Similarity 37.5%; Pred. No. 2.1e+03;
 Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 NFYKLPQM 11
 | | : |
 Db 1 NLYQFKNM 8

RESULT 27

BTID_BOOMI

ID BTID_BOOMI STANDARD; PRT; 17 AA.
 AC P83607;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kunitz-type serine protease inhibitor BmTI-D (Fragment).
 OS Boophilus microplus (Cattle tick).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Parasitiformes; Ixodida; Ixodidae; Boophilus.
 OX NCBI_TaxID=6941;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=Larva;
 RA Sasaki S.D., Hirata I.Y., Tanaka A.S.;
 RT "Molecular studies of serine protease inhibitors from cattle tick
 RT Boophilus microplus (larvae).";
 RL Submitted (JUN-2003) to Swiss-Prot.
 CC -!- FUNCTION: Inhibits trypsin and human plasma kallikrein.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Contains 1 BPTI/Kunitz inhibitor domain.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; PARTIAL.
 DR PROSITE; PS50279; BPTI_KUNITZ_2; PARTIAL.
 KW Serine protease inhibitor.
 FT ACT_SITE 16 17 REACTIVE BOND (BY SIMILARITY).
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1649 MW; 7A151C7189F44BBB CRC64;

Query Match 29.0%; Score 18; DB 1; Length 17;
 Best Local Similarity 50.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NFYKLP 9
 : | | : |
 Db 3 DFSKVP 8

RESULT 28

NPMA_BOVIN

ID NPMA_BOVIN STANDARD; PRT; 18 AA.
 AC P15506;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Morphine modulating neuropeptide A.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain;
 RX MEDLINE=86067985; PubMed=3865193;
 RA Yang H.-Y.T., Fratta W., Majane E.A., Costa E.;
 RT "Isolation, sequencing, synthesis, and pharmacological
 RT characterization of two brain neuropeptides that modulate the action
 RT of morphine.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
 CC -!- FUNCTION: Modulates the action of morphine.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 DR PIR; A24749; A24749.
 KW Neuropeptide; Amidation.
 FT MOD_RES 18 18 AMIDATION.
 SQ SEQUENCE 18 AA; 1921 MW; EC52DAE1F45CFCFB CRC64;

Query Match 29.0%; Score 18; DB 1; Length 18;
 Best Local Similarity 75.0%; Pred. No. 2.4e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PQNF 5
 |||
 Db 15 PQRF 18

RESULT 29

TKC1_CALVO

ID TKC1_CALVO STANDARD; PRT; 9 AA.
 AC P41517;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Callitachykinin I.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RX MEDLINE=95075727; PubMed=7984492;
 RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,
 RA Naessel D.R.;
 RT "Callitachykinin I and II, two novel myotropic peptides isolated from
 RT the blowfly, Calliphora vomitoria, that have resemblances to

RT tachykinins.";
RL Peptides 15:761-768(1994).
CC -!- FUNCTION: Myoactive peptide.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 981 MW; 2417C86B59CDC1B7 CRC64;

Query Match 27.4%; Score 17; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFY 6
| |
Db 2 PTAFY 6

RESULT 30

FAR6_PANRE

ID FAR6_PANRE STANDARD; PRT; 10 AA.
AC P82660;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE FMRFamide-like neuropeptide PF6 (NGAPQPFVRF-amide).
OS Panagrellus redivivus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
OX NCBI_TaxID=6233;
RN [1]
RP SEQUENCE, FUNCTION, AND AMIDATION.
RA Moffett C.L., Marks N.J., Halton D.W., Thomson D.P., Geary T.G.,
RA Maule A.G.;
RT "Isolation, characterization and pharmacology of RMRFamide-related
peptides (FaRPs) from free-living nematode, Panagrellus redivivus.";
RL Submitted (JUL-2000) to Swiss-Prot.
CC -!- FUNCTION: Myoactive.
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
family.
KW Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1132 MW; CB13E4C9D776C76D CRC64;

Query Match 27.4%; Score 17; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYK 7
| | | :
Db 4 PQPFVR 9

RESULT 31

CKX_WHEAT

ID CKX_WHEAT STANDARD; PRT; 15 AA.
AC P58763;

DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Cytokinin dehydrogenase (EC 1.5.99.12) (CKO) (CKX) (Fragment).
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE, AND CHARACTERIZATION.
 RC STRAIN=cv. Samantha;
 RX MEDLINE=21099312; PubMed=11168382;
 RA Galuszka P., Frebort I., Sebela M., Sauer P., Jacobsen S., Pec P.;
 RT "Cytokinin oxidase or dehydrogenase? Mechanism of cytokinin
 RT degradation in cereals.";
 RL Eur. J. Biochem. 268:450-461(2001).
 CC -!- FUNCTION: Catalyzes the oxidation of cytokinins, a family of N(6)-
 CC substituted adenine derivatives that are plant hormones, where the
 CC substituent is an isopentenyl group. Substrate preference is 2-(2-
 CC Hydroxyethylamino)-9-methyl-N(6)-isopentenyladenine >>
 CC isopentenyladenine > cis-zeatin = isopentenyladenosine = zeatin >>
 CC zeatin riboside.
 CC -!- CATALYTIC ACTIVITY: N(6)-dimethylallyl-adenine + electron acceptor
 CC = adenine + 3-methylbut-2-enal + reduced electron acceptor +
 CC H(2)O.
 CC -!- COFACTOR: FAD.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Might be located on membranes.
 CC -!- MISCELLANEOUS: Optimal pH is 6.5.
 KW Oxidoreductase; Flavoprotein; FAD.
 FT UNSURE 1 1
 FT UNSURE 13 15
 FT NON TER 15 15
 SQ SEQUENCE 15 AA; 1709 MW; 85B589BD53FCEDEF CRC64;

 Query Match 27.4%; Score 17; DB 1; Length 15;
 Best Local Similarity 25.0%; Pred. No. 3.1e+03;
 Matches 2; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

 QY 1 MPQNFYKL 8
 :|:: :|
 Db 2 LPKSLFTL 9

RESULT 32

FMF1_ECOLI
 ID FMF1_ECOLI STANDARD; PRT; 18 AA.
 AC P20860;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE F7-1 fimbrial protein (F7-1 pilin) (P adhesin) (Fragment).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;

RN [1]
 RP SEQUENCE.
 RX MEDLINE=89079313; PubMed=2562836;
 RA Hoschuetzky H., Lottspeich F., Jann K.;
 RT "Isolation and characterization of the alpha-galactosyl-1,4-beta-
 RT galactosyl-specific adhesin (P adhesin) from fimbriated Escherichia
 RT coli.";
 RL Infect. Immun. 57:76-81(1989).
 CC -!- FUNCTION: Fimbriae (also called pili), polar filaments radiating
 CC from the surface of the bacterium to a length of 0.5-1.5
 CC micrometers and numbering 100-300 per cell, enable bacteria to
 CC colonize the epithelium of specific host organs.
 CC -!- MISCELLANEOUS: This is an alpha-galactosyl-1,4-beta-galactosyl-
 CC specific adhesin.
 DR PIR; A30541; A30541.
 KW Fimbria.
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 1956 MW; E9A44CDA6E2886B5 CRC64;

 Query Match 27.4%; Score 17; DB 1; Length 18;
 Best Local Similarity 75.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 5 FYKL 8
 |||
 Db 6 FYSL 9

RESULT 33

HEMH_THETS

ID HEMH_THETS STANDARD; PRT; 18 AA.
 AC P80155;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ovohemerythrin (YP14) (Fragment).
 OS Theromyzon tessulatum (Leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
 OX NCBI_TaxID=13286;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Oocyte;
 RX MEDLINE=93049299; PubMed=1425663;
 RA Baert J.-L., Britel M., Sautiere P., Malecha J.;
 RT "Ovohemerythrin, a major 14-kDa yolk protein distinct from
 RT vitellogenin in leech.";
 RL Eur. J. Biochem. 209:563-569(1992).
 CC -!- FUNCTION: Major yolk protein. This iron protein may play a role
 CC in the detoxification of free iron after a blood meal.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the hemerythrin family.
 DR PIR; S29264; S29264.
 DR HSSP; P02247; 2MHR.
 DR InterPro; IPR002063; Hemerythrin.
 DR Pfam; PF01814; Hemerythrin; 1.
 DR PROSITE; PS00550; HEMERYTHRINS; PARTIAL.

KW Oxygen transport; Metal-binding; Iron; Yolk.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2368 MW; 33397EEE587C81F1 CRC64;

Query Match 27.4%; Score 17; DB 1; Length 18;
Best Local Similarity 40.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 YKLPQ 10
| :|:
Db 1 YDIPE 5

RESULT 34

LUXB_KRYAS

ID LUXB_KRYAS STANDARD; PRT; 18 AA.
AC P18300;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Alkanal monooxygenase beta chain (EC 1.14.14.3) (Bacterial luciferase
DE beta chain) (Fragment).
GN LUXB.
OS Kryptophanaron alfredi symbiont.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; light emitting symbionts of fish.
OX NCBI_TaxID=28177;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91076680; PubMed=2256783;
RA Haygood M.G.;
RT "Relationship of the luminous bacterial symbiont of the Caribbean
RT flashlight fish, Kryptophanaron alfredi (family Anomalopidae) to
RT other luminous bacteria based on bacterial luciferase (luxA) genes."
RL Arch. Microbiol. 154:496-503(1990).
CC -!- FUNCTION: LIGHT-EMITTING REACTION IN LUMINOUS BACTERIA. THE
CC SPECIFIC ROLE OF THE BETA SUBUNIT IS UNKNOWN, BUT IT IS ABSOLUTELY
CC REQUIRED FOR BIOLUMINESCENCE ACTIVITY.
CC -!- CATALYTIC ACTIVITY: RCHO + FMNH(2) + O(2) = RCOOH + FMN + H(2)O +
CC light.
CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.
CC -----
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CC -----
DR EMBL; M36597; AAA91214.1; -.
DR InterPro; IPR002103; Bac luciferase.
DR PROSITE; PS00494; BACTERIAL_LUCIFERASE; PARTIAL.
KW Photoprotein; Luminescence; Oxidoreductase; Monooxygenase;
KW Flavoprotein; FMN.
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2153 MW; 8CB3B6955CCB2E7A CRC64;

Query Match 27.4%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QNF 5
|||
Db 8 QNF 10

RESULT 35

BUK_CLOPA

ID BUK_CLOPA STANDARD; PRT; 9 AA.
AC P81337;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Butyrate kinase (EC 2.7.2.7) (BK) (CP 38) (Fragment).
GN BUK.
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengsrud R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -!- FUNCTION: Catalyzes the conversion of butyryl-CoA through butyryl
CC phosphate to butyrate (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + 2-butanolate = ADP + butanoyl phosphate.
CC -!- PATHWAY: Involved in the acidogenic phase of fermentation.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the acetokinase family.
DR HAMAP; MF_00542; -; 1.
DR InterPro; IPR000890; Acetate_kin.
DR PROSITE; PS01075; ACETATE_KINASE_1; PARTIAL.
DR PROSITE; PS01076; ACETATE_KINASE_2; PARTIAL.
KW Transferase; Kinase.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1104 MW; 055D40505727232B CRC64;

Query Match 25.8%; Score 16; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YKL 8
|||
Db 2 YKL 4

RESULT 36

HUTU_KLEAE

ID HUTU_KLEAE STANDARD; PRT; 9 AA.

AC P12381;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Urocanate hydratase (EC 4.2.1.49) (Urocanase) (Imidazolonepropionate
 DE hydrolase) (Fragment).
 GN HUTU.
 OS Klebsiella aerogenes.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Klebsiella.
 OX NCBI_TaxID=28451;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88198018; PubMed=2834335;
 RA Nieuwkoop A.J., Baldauf S.A., Hudspeth M.E.S., Bender R.A.;
 RT "Bidirectional promoter in the hut(P) region of the histidine
 RT utilization (hut) operons from Klebsiella aerogenes.";
 RL J. Bacteriol. 170:2240-2246(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90368611; PubMed=2203754;
 RA Schwacha A., Bender R.A.;
 RT "Nucleotide sequence of the gene encoding the repressor for the
 RT histidine utilization genes of Klebsiella aerogenes.";
 RL J. Bacteriol. 172:5477-5481(1990).
 CC -!- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-3-H-imidazol-4-
 CC yl)propanoate = urocanate + H(2)O.
 CC -!- COFACTOR: Binds 1 NAD per subunit (By similarity).
 CC -!- PATHWAY: Histidine degradation; second step.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to the urocanase family.
 CC -----
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 CC -----
 DR EMBL; M19665; AAA25078.1; -.
 DR EMBL; M34604; AAA25076.1; -.
 DR HAMAP; MF_00577; -; 1.
 DR InterPro; IPR000193; Urocanase.
 DR PROSITE; PS01233; UROCANASE; PARTIAL.
 KW Histidine metabolism; Lyase; NAD.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1140 MW; 970FC41B5325A6C5 CRC64;

Query Match 25.8%; Score 16; DB 1; Length 9;
 Best Local Similarity 42.9%; Pred. No. 1.4e+05;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MPQNFYK 7
 | | : | :
 Db 1 MSQSKYR 7

RESULT 37

CATB_SHEEP

ID CATB_SHEEP STANDARD; PRT; 10 AA.
 AC P83205;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cathepsin B (EC 3.4.22.1) (Cathepsin B1) (Fragment).
 GN CTSB.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Placenta;
 RX MEDLINE=22394055; PubMed=12506352;
 RA El Amiri B., Remy B., Sousa N.M., Joris B., Ottiers N.G., Perenyi Z.,
 RA Mboko H.B., Beckers J.-F.M.P.;
 RT "Isolation and partial characterization of three pregnancy-associated
 RT glycoproteins from the ewe placenta."
 RL Mol. Reprod. Dev. 64:199-206(2003).
 CC -!- FUNCTION: Thiol protease which is believed to participate in
 CC intracellular degradation and turnover of proteins. Has also been
 CC implicated in tumor invasion and metastasis.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity
 CC for peptide bonds. Preferentially cleaves -Arg-Arg-|-Xaa bonds in
 CC small molecule substrates (thus differing from cathepsin L). In
 CC addition to being an endopeptidase, shows peptidyl-dipeptidase
 CC activity, liberating C-terminal dipeptides.
 CC -!- SUBUNIT: Dimer of a heavy chain and a light chain cross-linked
 CC by a disulfide bond (By similarity).
 CC -!- SUBCELLULAR LOCATION: Lysosomal (By similarity).
 CC -!- SIMILARITY: Belongs to peptidase family C1.
 DR InterPro; IPR000169; SHprot_acsite.
 DR PROSITE; PS00640; THIOLEPROTEASE_ASN; PARTIAL.
 DR PROSITE; PS00139; THIOLEPROTEASE_CYS; PARTIAL.
 DR PROSITE; PS00639; THIOLEPROTEASE_HIS; PARTIAL.
 KW Hydrolase; Thiol protease; Lysosome.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1177 MW; 8795780DDAA9D5BA CRC64;

Query Match 25.8%; Score 16; DB 1; Length 10;
 Best Local Similarity 40.0%; Pred. No. 3.1e+03;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPQNF 5
 :| :|
 Db 1 LPDSF 5

RESULT 38

TKNB_RANCA

ID TKNB_RANCA STANDARD; PRT; 10 AA.
 AC P22689;

DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranatachykinin B (RTK B).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain;
 RX MEDLINE=91254337; PubMed=2043143;
 RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
 RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
 RT brain and intestine.";
 RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=94023216; PubMed=8210506;
 RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
 RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
 RT intestine.";
 RL Regul. Pept. 46:81-88(1993).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; B61033; B61033.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1210 MW; 917E556B59D5BAB5 CRC64;

Query Match 25.8%; Score 16; DB 1; Length 10;
 Best Local Similarity 60.0%; Pred. No. 3.1e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NFYKL 8
 :|||
 Db 5 SFYGL 9

RESULT 39

CXL1_CONMR

ID CXL1_CONMR STANDARD; PRT; 11 AA.
 AC P58807;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lambda-conotoxin CMrVIA.
 OS Conus marmoreus (Marble cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;

OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=42752;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=20564325; PubMed=10988292;
 RA Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
 RA Seow K.T., Bay B.-H.;
 RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide
 RT pattern and protein folding. Isolation and characterization from the
 RT venom of Conus marmoreus.";
 RL J. Biol. Chem. 275:39516-39522(2000).
 CC -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- MASS SPECTROMETRY: MW=1237.93; MW_ERR=0.21; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
 KW Neurotoxin; Toxin; Hydroxylation.
 FT DISULFID 2 11
 FT DISULFID 3 8
 FT MOD_RES 10 10 HYDROXYLATION.
 SQ SEQUENCE 11 AA; 1226 MW; 277AAC60B7232B58 CRC64;

Query Match 25.8%; Score 16; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YKL 8
 |||
 Db 5 YKL 7

RESULT 40

TKNA_SCYCA

ID TKNA_SCYCA STANDARD; PRT; 11 AA.
 AC P41333;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Substance P.
 OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
 OC Scyliorhinidae; Scyliorhinus.
 OX NCBI_TaxID=7830;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=93292508; PubMed=7685693;
 RA Waugh D., Wang Y., Hazon N., Balment R.J., Conlon J.M.;
 RT "Primary structures and biological activities of substance-P-related
 RT peptides from the brain of the dogfish, Scyliorhinus canicula.";
 RL Eur. J. Biochem. 214:469-474(1993).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.

CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S33300; S33300.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1278 MW; 214860DEC9D6D867 CRC64;

Query Match 25.8%; Score 16; DB 1; Length 11;
Best Local Similarity 42.9%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PQNFYKL 8
| |:
Db 4 PGQFFGL 10

RESULT 41

PPK4_PERAM

ID PPK4_PERAM STANDARD; PRT; 12 AA.
AC P82619;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-4 (Pea-PK-4) (YXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Retrocerebral complex;
RX MEDLINE=99212469; PubMed=10196736;
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
RT "Differential distribution of pyrokinin-isoforms in cerebral and
RT abdominal neurohemal organs of the American cockroach."
RL Insect Biochem. Mol. Biol. 29:139-144(1999).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
RT the American cockroach."
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -!- TISSUE SPECIFICITY: Corpora cardiaca.
CC -!- MASS SPECTROMETRY: MW=1147.9; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the pyrokinin family.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1449 MW; FA7A3049FF42CAA1 CRC64;

Query Match 25.8%; Score 16; DB 1; Length 12;
Best Local Similarity 33.3%; Pred. No. 3.7e+03;

Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MPQNFY 6
:| :|
Db 3 LPHDVY 8

RESULT 42

CRTC_RANES

ID CRTC_RANES STANDARD; PRT; 13 AA.
AC P31832;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Calreticulin (Major microsomal calcium-binding protein) (Fragment).
OS Rana esculenta (Edible frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8401;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91207333; PubMed=2018493;
RA Treveso S., Zorzato F., Chiozzi P., Melandri P., Volpe P., Pozzan T.;
RT "Frog brain expresses a 60 KDa Ca2+ binding protein similar to
RT mammalian calreticulin.";
RL Biochem. Biophys. Res. Commun. 175:444-450(1991).
CC -!- FUNCTION: This protein binds calcium. There are both high and low
CC affinity calcium-binding sites.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the calreticulin family.
DR InterPro; IPR001580; Calreticulin.
DR PROSITE; PS00803; CALRETICULIN_1; PARTIAL.
DR PROSITE; PS00804; CALRETICULIN_2; PARTIAL.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; PARTIAL.
KW Endoplasmic reticulum; Calcium-binding.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1510 MW; D0F62AD09EAEE339 CRC64;

Query Match 25.8%; Score 16; DB 1; Length 13;

Best Local Similarity 50.0%; Pred. No. 4e+03;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PQNFYK 7
| |:
Db 2 PLVFFK 7

RESULT 43

CXL4_CONMR

ID CXL4_CONMR STANDARD; PRT; 13 AA.
AC P58810;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lambda/chi-conotoxin MrIB (Chi-MrIB).
OS Conus marmoreus (Marble cone).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=42752;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND STRUCTURE BY NMR.
 RC TISSUE=Venom;
 RX MEDLINE=21419681; PubMed=11528421;
 RA Sharpe I.A., Gehrmann J., Loughnan M.L., Thomas L., Adams D.A.,
 RA Atkins A., Palant E., Craik D.J., Adams D.J., Alewood P.F.,
 RA Lewis R.J.;
 RT "Two new classes of conopeptides inhibit the alphas-adrenoceptor and
 RT noradrenaline transporter.";
 RL Nat. Neurosci. 4:902-907(2001).
 CC -!- FUNCTION: Inhibits the neuronal noradrenaline transporter.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -!- PTM: Exists in two forms, due to cis-trans isomerization at His-
 CC 11-Hyp-12.
 CC -!- MASS SPECTROMETRY: MW=1393.52; METHOD=Electrospray.
 CC -!- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
 DR PDB; 1IEO; 03-APR-02.
 KW Neurotoxin; Toxin; Hydroxylation; 3D-structure.
 FT DISULFID 4 13
 FT DISULFID 5 10
 FT MOD_RES 12 12 HYDROXYLATION.
 SQ SEQUENCE 13 AA; 1382 MW; 277AAC376EAD2B58 CRC64;

 Query Match 25.8%; Score 16; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 6 YKL 8
 |||
 Db 7 YKL 9

RESULT 44

SMS1_MYOSC

ID SMS1_MYOSC STANDARD; PRT; 14 AA.
 AC P20750;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Somatostatin I.
 OS Myoxocephalus scorpius (Shorthorn sculpin) (Daddy sculpin),
 OS Oncorhynchus kisutch (Coho salmon), and
 OS Anguilla anguilla (European freshwater eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
 OC Cottoidei; Cottidae; Myoxocephalus.
 OX NCBI_TaxID=8097, 8019, 7936;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=M.scorpius; TISSUE=Pancreas;
 RX MEDLINE=88029486; PubMed=2889597;

RA Conlon J.M., Davis M.S., Falkmer S., Thim L.;
 RT "Structural characterization of peptides derived from
 RT prosomatostatins I and II isolated from the pancreatic islets of two
 RT species of teleostean fish: the daddy sculpin and the flounder.";
 RL Eur. J. Biochem. 168:647-652(1987).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=O.kisutch; TISSUE=Pancreas;
 RX MEDLINE=87055212; PubMed=2877919;
 RA Plisetskaya E.M., Pollock H.G., Rouse J.B., Hamilton J.W.,
 RA Kimmel J.R., Andrews P.C., Gorbman A.;
 RT "Characterization of coho salmon (*Oncorhynchus kisutch*) islet
 RT somatostatins.";
 RL Gen. Comp. Endocrinol. 63:252-263(1986).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=A.anguilla; TISSUE=Pancreas;
 RX MEDLINE=89065329; PubMed=2904391;
 RA Conlon J.M., Deacon C.F., Hazon N., Henderson I.W., Thim L.;
 RT "Somatostatin-related and glucagon-related peptides with unusual
 RT structural features from the European eel (*Anguilla anguilla*).";
 RL Gen. Comp. Endocrinol. 72:181-189(1988).
 CC -!- FUNCTION: Somatostatin inhibits the release of somatotropin.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the somatostatin family.
 DR PIR; A60840; A60840.
 DR PIR; B60842; B60842.
 DR PIR; S00172; S00172.
 DR InterPro; IPR004250; Somatostatin.
 DR Pfam; PF03002; Somatostatin; 1.
 KW Hormone; Multigene family.
 FT DISULFID 3 14
 SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;

Query Match 25.8%; Score 16; DB 1; Length 14;
 Best Local Similarity 50.0%; Pred. No. 4.4e+03;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QNFY 6
 :||:
 Db 4 KNFF 7

RESULT 45

SMS_ALLMI

ID SMS_ALLMI STANDARD; PRT; 14 AA.
 AC P31885;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Somatostatin-14.
 OS Alligator mississippiensis (American alligator), and
 OS Trachemys scripta (Red-eared slider turtle) (*Pseudemys scripta*).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
 OX NCBI_TaxID=8496, 34903;
 RN [1]

RP SEQUENCE.
 RC SPECIES=A.mississippiensis; TISSUE=Stomach;
 RX MEDLINE=93324451; PubMed=8101369;
 RA Wang Y., Conlon J.M.;
 RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
 RT and stomach of the alligator.";
 RL Peptides 14:573-579(1993).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=T.scripta;
 RX MEDLINE=90341082; PubMed=1974347;
 RA Conlon J.M., Hicks J.W.;
 RT "Isolation and structural characterization of insulin, glucagon and
 RT somatostatin from the turtle, Pseudemys scripta.";
 RL Peptides 11:461-466(1990).
 CC -!- FUNCTION: Somatostatin inhibits the release of somatotropin.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the somatostatin family.
 DR PIR; C60414; C60414.
 DR InterPro; IPR004250; Somatostatin.
 DR Pfam; PF03002; Somatostatin; 1.
 KW Hormone.
 FT DISULFID 3 14 BY SIMILARITY.
 SQ SEQUENCE 14 AA; 1640 MW; D6270F5C09682679 CRC64;

Query Match 25.8%; Score 16; DB 1; Length 14;
 Best Local Similarity 50.0%; Pred. No. 4.4e+03;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QNFY 6
 :||:
 Db 4 KNFF 7

RESULT 46

TKNM_RANMA
 ID TKNM_RANMA STANDARD; PRT; 14 AA.
 AC P40951;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranamargarin.
 OS Rana margaratae (Chinese frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=121156;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=90026852; PubMed=2803524;
 RA Tang Y.Q., Tian S.H., Wu S.X., Hua J.C., Wu G.F., Zhao E.M., Lu Y.A.,
 RA Zhu Y.Q., Zou G., Tsou K.;
 RT "Isolation and structure of ranamargarin, a new tachykinin from the
 RT skin of Chinese frog Rana margaratae.";
 RL Sci. China, Ser. B, Chem. Life Sci. Earth Sci. 32:570-579(1989).
 RN [2]
 RP SYNTHESIS.

RX MEDLINE=90253600; PubMed=2340087;
 RA Lu Y.A., Peng J.L., Zhu Y.Q., Wu S.X., Tang Y.Q., Tian S.H., Zou G.;
 RT "Synthesis and biological activity of a new frog skin peptide,
 RT ranamargarin.";
 RL Sci. China, Ser. B, Chem. Life Sci. Earth Sci. 33:170-177(1990).
 CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 14 14 AMIDATION.
 SQ SEQUENCE 14 AA; 1617 MW; D4593AE408C3673D CRC64;

Query Match 25.8%; Score 16; DB 1; Length 14;
 Best Local Similarity 50.0%; Pred. No. 4.4e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 QNFYKL 8
 : || |
 Db 8 KKFYGL 13

RESULT 47

GTS_ASADI

ID GTS_ASADI STANDARD; PRT; 15 AA.
 AC P83246;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glutathione S-transferase (EC 2.5.1.18) (GST class-sigma) (adGST)
 DE (Fragment).
 OS Asaphis dichotoma.
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
 OC Tellinoidea; Psammobiidae; Asaphis.
 OX NCBI_TaxID=184428;
 RN [1]
 RP SEQUENCE, FUNCTION, SUBUNIT, MASS SPECTROMETRY, AND CIRCULAR DICHROISM
 RP ANALYSIS.
 RC TISSUE=Intestine, and Liver;
 RX MEDLINE=22135252; PubMed=12139969;
 RA Yang H.-L., Nie L.-J., Zhu S.-G., Zhou X.-W.;
 RT "Purification and characterization of a novel glutathione S-
 RT transferase from Asaphis dichotoma.";
 RL Arch. Biochem. Biophys. 403:202-208(2002).
 CC -!- FUNCTION: Has a strong specific activity toward 1-chloro-2,4-
 CC dinitrobenzene and etharynic acid.
 CC -!- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
 CC -!- SUBUNIT: Homodimer.
 CC -!- MASS SPECTROMETRY: MW=23138; METHOD=MALDI.
 CC -!- MISCELLANEOUS: In A.dichotoma there are at least two isozymes of
 CC glutathione S-transferase.
 CC -!- MISCELLANEOUS: Optimal pH is 8.5 with 1-chloro-2,4-dinitrobenzene

CC as the substrate.
 CC -!- MISCELLANEOUS: The Km for 1-chloro-2,4-dinitrobenzene and
 CC glutathione are 0.68 +/-0.05 and 0.106 +/-0.005 mM, and the Vmax
 CC is 0.1446 +/-0.0072 and 0.033 +/-0.002 mmol/min x mg enzyme,
 CC respectively.
 CC -!- SIMILARITY: Belongs to the GST superfamily. Sigma family.
 DR GO; GO:0004364; F:glutathione transferase activity; NAS.
 DR GO; GO:0006803; P:glutathione conjugation reaction; NAS.
 KW Transferase.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1767 MW; CB3E4BF92D3CB0B9 CRC64;

Query Match 25.8%; Score 16; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 YKL 8
 |||
 Db 3 YKL 5

RESULT 48

LEC1_PSOSC

ID LEC1_PSOSC STANDARD; PRT; 15 AA.
 AC P22582;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Acidic lectin A1 (Fragment).
 OS Psophocarpus scandens.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 OC Psophocarpus.
 OX NCBI_TaxID=3890;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Seed;
 RA Kortt A.A.;
 RT "Isolation and characterization of the lectins from the seeds of
 RT Psophocarpus scandens.";
 RL Phytochemistry 27:2847-2855(1988).
 CC -!- SUBUNIT: DIMER. THE SUBUNITS SHOW APPARENT MW HETEROGENEITY
 CC (32000-35000 MW), WHICH MAY RESULT FROM DIFFERENT CARBOHYDRATE
 CC CONTENT, AA SEQUENCE, OR POLYPEPTIDE LENGTH.
 CC -!- PTM: CONTAINS 5-6% CARBOHYDRATE.
 CC -!- SIMILARITY: WITH P.TETRAGONOLOBUS ACIDIC LECTINS IN N-TERMINAL
 CC SEQUENCE, AA COMPOSITION, ERYTHROCYTE AND SUGAR SPECIFICITIES.
 DR PIR; PA0005; PA0005.
 KW Lectin; Glycoprotein.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1743 MW; D6EB9FE9C6B0254D CRC64;

Query Match 25.8%; Score 16; DB 1; Length 15;
 Best Local Similarity 50.0%; Pred. No. 4.7e+03;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPQN 4
:|:|
Db 12 VPEN 15

RESULT 49

MCA2_RHOOP

ID MCA2_RHOOP STANDARD; PRT; 15 AA.
AC P56870;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative maleylacetate reductase II (EC 1.3.1.32) (Fragment).
OS Rhodococcus opacus (Nocardia opaca).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=37919;
RN [1]
RP SEQUENCE.
RC STRAIN=1CP;
RX MEDLINE=98324954; PubMed=9657989;
RA Seibert V., Kourbatova E.M., Golovleva L.A., Schloemann M.;
RT "Characterization of a maleylacetate reductase encoding region from
RT Rhodococcus opacus 1CP.";
RL J. Bacteriol. 180:3503-3508(1998).
CC -!- CATALYTIC ACTIVITY: 3-oxoadipate + NAD(P)(+) = 2-maleylacetate +
CC NAD(P)H.
CC -!- PATHWAY: 3-chlorocatechol degradation (beta-ketoadipate pathway).
CC THIS PATHWAY SERVES A VITAL ROLE IN THE BIODEGRADATION OF TOXIC
CC AROMATIC COMPOUNDS INTRODUCED IN THE ENVIRONMENT BOTH AS NATURAL
CC PRODUCTS AND AS INDUSTRIAL EFFLUENT.
CC -!- SIMILARITY: Belongs to the iron-containing alcohol dehydrogenase
CC family.
DR InterPro; IPR001670; Fe-ADH.
DR PROSITE; PS00913; ADH_IRON_1; PARTIAL.
DR PROSITE; PS00060; ADH_IRON_2; PARTIAL.
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1884 MW; 58DA90DD038F025E CRC64;

Query Match 25.8%; Score 16; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LPQ 10
|||
Db 8 LPQ 10

RESULT 50

AF1S_MALPA

ID AF1S_MALPA STANDARD; PRT; 16 AA.
AC P83140;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Antifungal protein 1 small subunit (CW-1) (Fragment).

OS Malva parviflora (Little mallow) (Cheeseweed).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Malva.
 OX NCBI_TaxID=145753;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=Seed;
 RX MEDLINE=20568734; PubMed=11118343;
 RA Wang X., Bunkers G.J.;
 RT "Potent heterologous antifungal proteins from cheeseweed (Malva
 RT parviflora).";
 RL Biochem. Biophys. Res. Commun. 279:669-673(2000).
 CC -!- FUNCTION: Possesses antifungal activity against F.graminearum.
 CC -!- SUBUNIT: Heterodimer of a large and a small subunit.
 CC -!- MISCELLANEOUS: Antimicrobial activity is not affected by salt
 CC concentration.
 DR GO; GO:0003799; F:antifungal peptide activity; IDA.
 KW Fungicide; Antibiotic.
 FT NON TER 16 16
 SQ SEQUENCE 16 AA; 1888 MW; 2893A1C66F5D3F57 CRC64;

Query Match 25.8%; Score 16; DB 1; Length 16;
 Best Local Similarity 25.0%; Pred. No. 5e+03;
 Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PQNFYKLP 9
 | :::|
 Db 1 PAGPFRIP 8

Search completed: July 4, 2004, 04:41:30
 Job time : 4.77612 secs